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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/EP99/05652 <b>(22) International Filing Date:</b> 4 August 1999 (04.08.99) <b>(30) Priority Data:</b> 98202634.6 4 August 1998 (04.08.98) EP <b>(71) Applicant (for all designated States except US):</b> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijvisschestraat 120, B-9052 Zwij- naarde (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). <b>(74) Agent:</b> DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished          upon receipt of that report.</i>
<b>(54) Title:</b> GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS  <b>(57) Abstract</b> <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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### Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant  
5 molecular biology. In particular, the invention relates to improvements of crop  
productivity of useful plants. One of the major limitations of crop productivity is the  
effect of environmental stress conditions on plant growth and development. An  
important goal of molecular biology is the identification and isolation of genes that can  
provide resistance or tolerance to such stresses. For agriculture, the creation of  
10 transgenic plants containing such genes provides the potential for improving the stress  
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on  
the growth of plants and the productivity of crops. The physiological response to these  
stresses arises out of changes in cellular gene expression. Expression of a number of  
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;  
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be  
classified into two groups: those that directly protect against environmental stresses  
and those that regulate gene expression and signal transduction in the stress  
response. The first group includes proteins that likely function by protecting cells from  
20 dehydration, such as the enzymes required for biosynthesis of various  
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,  
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,  
Bray et al., 1997). The second group of gene products includes transcription factors,  
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et  
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is  
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms  
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the  
30 hypothesis that the genetic information for tolerance to environmental stress conditions  
exists in all higher plants. In glycophytes, this information would only be expressed in  
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:  
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of  
35 evidence also demonstrate that even mild environmental stress conditions throughout  
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively-easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO<sub>2</sub> etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole  
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium  
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence  
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth  
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,  
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the  
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 $\mu$  plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5       The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10       The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15       The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20       (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25       (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30       Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which  
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent  
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1  
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or  
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having  
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid  
30 comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,  
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DBF2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;



- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

5  
10 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more  
15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

20 Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74,  
25 more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

30

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not  
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the  
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence  
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means  
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of  
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and  
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially  
5 identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be  
10 produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et  
15 al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide  
20 encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at  
25 least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a  
30 recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least  
35 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5       The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10       The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression in these systems.

15       The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress of said plant.

20       The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

25       The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

30       Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably  
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method  
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a  
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a  
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a  
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,  
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said  
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced  
5 tolerance or resistance to environmental stress, said method comprising indirectly  
increasing or inducing the expression of an endogenous gene in said plant comprised  
within a polynucleic acid as defined above or indirectly increasing or inducing the activity  
of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

10 (a) introducing into the genome of a plant cell one or more recombinant DNA  
molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in  
said plant cell at an effective amount indirectly  
increases or induces the expression of an  
15 endogenous polynucleic acid or indirectly increases  
or induces the protein activity of a protein encoded by  
said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in  
the same transcriptional unit and under the control of  
said plant-expressible promoter, and,

20 (b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence"  
meaning that said recombinant DNA molecule will comprise a sequence originating  
from a foreign species, or, if from the same species, may be substantially modified  
25 from its original form. For example, a promoter operably linked to a structural gene  
which is from a species different from which the structural gene was derived, or, if  
from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing  
a plant with enhanced tolerance or resistance to environmental stress conditions, said  
30 method comprising indirectly increasing or inducing the expression of an endogenous  
gene in said plant comprised within a polynucleic acid as defined above or indirectly  
increasing or inducing the activity of a protein of the invention as defined above.  
According to this embodiment, other polynucleic acids modulating the expression or  
the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.



For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of  
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,  
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of  
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and  
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example  
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The  
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with  
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of  
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose  
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the  
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control  
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard  
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in  
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,  
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter  
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,  
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the  
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannisetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative  
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a  
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can  
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,  
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

25 Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress  
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of  
35 the present invention can be employed to produce transgenic stress tolerant plant with



any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardia glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5       The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10       The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein  
15       having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

20       The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present  
25       invention also relates to the coding region as well as the promoter region of any of said genomic clones.

      The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30       The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the  
35       primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references  
5 mentioned herein are incorporated by reference.

## BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast Dbf2 (A)  
 Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*.  
 5 Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2*  
 sequence indicate the protein kinase catalytic subdomains defined by Hanks et al.  
 (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3*  
*ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of  
 daughter cells (dumbbells) at restrictive temperature (37° C). The defective  
 10 morphology of the *dbf2* mutant can be complemented by transformation with the  
 pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA  
 (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log  
 phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After  
 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas  
 15 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly  
 provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to  
 osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density  
 20 was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing  
*DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing  
*At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step 1:10. Ten µl of each dilution  
 was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic  
 stress) or 1.2 M NaCl (salt stress) or 4µl H<sub>2</sub>O<sub>2</sub> (oxidative stress) and incubated at 28°C  
 25 or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis  
 showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and  
 the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern  
 30 analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as  
 described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl  
 1% (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6); and of *DBF2* in yeast cells grown for 11/2  
 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with  
 0.4 mM H<sub>2</sub>O<sub>2</sub> (6). Control of loading has been done with EtBr staining and is shown  
 35 under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5           Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to  
10   OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

          Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during  
15   plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown  
20   in b and d using a Phosphorimager (Molecular Dynamics).

          Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
25   section) upon applying a salt stress of 200 mM NaCl overnight.

          Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
30   section) upon applying an osmotic stress induced by 20% PEG overnight.

          Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H<sub>2</sub>O<sub>2</sub>, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H<sub>2</sub>O<sub>2</sub> (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.



Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

## EXAMPLES

### **Example 1. Construction of the cDNA library.**

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM Tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H<sub>2</sub>O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)<sub>14</sub>-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

### **Example 2. Yeast transformation and selection for osmotolerance.**

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schieters, 1995). After transformation with the *Arabidopsis* cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected *Arabidopsis* cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected *Arabidopsis* cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD<sub>600</sub> at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

### Example 3. Characterization of *At-DBF2*.

*At-DBF2*, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward et al. 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks et al. (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

10

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

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### Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

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In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

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time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive  
5 role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

10 **Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-BDF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the  
15 overexpression of both *DBF2* and *At-DBF2* (Figure 4).

**Example 6. *At-DBF2* is cell cycle regulated.**

*DBF2* expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4  
20 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S  
25 phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases  
30 until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerns *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

**Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction**

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

**Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells**

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

**Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress**

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the *gfp* receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

**Example 10. Tolerance to environmental stress in plant cells**

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-*CaMVter*. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

#### Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefore seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,



70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l<sup>-1</sup> sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

#### Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm<sup>-3</sup> denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA.

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

**Tabel 1**

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dictyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent - kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 - sequence	107	+++	++++
unknown	chromosome 4 - sequence	109	+	++++
unknown	chromosome 5 - sequence	111	++++	+++
unknown	chromosome 5 - sequence	113	++++	++
unknown	chromosome 5 - sequence	115	++++	++++
unknown	chromosome 5 - sequence	117	+	++++
unknown	chromosome 5 - sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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**TABLE 2**  
**EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF**  
**THE PRESENT INVENTION**

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
$\alpha$ -amylase ( <i>Amy32b</i> )	Aleurone	Lanahan <i>et al.</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin $\beta$ -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	<a href="http://salus.medium.edu/mmq/tierney/html">http://salus.medium.edu/mmq/tierney/html</a>
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	<a href="http://salus.medium.edu/mmq/tierney/html">http://salus.medium.edu/mmq/tierney/html</a>
chalcone synthase ( <i>chsA</i> )	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; <a href="http://winetitles.com.au/gwrdc/csh95-1.html">http://winetitles.com.au/gwrdc/csh95-1.html</a>
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	<a href="http://salus.medium.edu/mmq/tierney/html">http://salus.medium.edu/mmq/tierney/html</a>
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform virus</i> gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
$\beta$ -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	<a href="http://salus.mediam.edu/mmg/tierney/html">http://salus.mediam.edu/mmg/tierney/html</a>
RD2 gene	root cortex	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
TobRB7 gene	root vasculature	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
AtPRP4	leaves; flowers; lateral root primordia	<a href="http://salus.mediam.edu/mmg/tierney/html">http://salus.mediam.edu/mmg/tierney/html</a>
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zeln	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
LEAFY	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993



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**Claims**

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
  - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
  - (a) SEQ ID NO 1, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

(a) SEQ ID NO 3, or the complementary strand thereof;

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

15

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

20

9. Use of an isolated polynucleic acid as defined above which is chosen from:

(a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

25

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

30

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

35

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- 5 (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined  
15 in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of  
SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40,  
42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,  
20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or  
120.

13. A method for producing a plant with enhanced tolerance or resistance to  
environmental stress, said method comprising transiently introducing into a plant  
25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of  
claims 2 to 10 which is expressed in an amount effective to confer enhanced  
tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to  
30 environmental stress, said method comprising stably introducing into a plant cell a  
recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2  
to 10 which is expressed in an amount effective to confer enhanced tolerance or  
resistance to environmental stress.



15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.

5

16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.

10

17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.

15

18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

20

- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
- a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

25

19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

30

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:  
a polynucleic acid according to or as defined in any of claims 2 to 10, and,  
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:  
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,  
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant  
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
24. The recombinant polynucleic acid of claim 21 comprising at least part of the  
30 nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
- 5 26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
- 10 28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
- 15 30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
- 20 32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
- 25 34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
- 35 35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.
- 35

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

At-DBF2	.....MAGNMSCLSTDGHGTPGGGHPNQNLTKRRTRPAGINDSPVVKCFPPYEDTSNTSLKEVSQPTKYSSNSPPVSPAI FYERATSWCT	89
DBF2	MLSKSEKNVDLLAGNMSNLSFDGHGTPGGTGLFPNQNLTKRRTRPAGINDSPVVKPSFFPYEDTSNMDIDEVSQPDMDVSNPKLPPKFYERATSNKT	100
At-DBF2	QRVVSGRAHYFLEYCDMFDYVISRRORTKQVLEYLQQSQQLPNSDQIKLNEEUSSYLOREHQVL SKRRLKPKNRD FEMITQVGGGGYGHVYLARKKDTK	189
DBF2	QRVVSVCKMYFLEHYCDMFDYVISRRORTKQVLEYLQQSQQLPNSDQIKLNEEUSSYLOREHQVL SKRRLKPKNRD FEMITQVGGGGYGHVYLARKKDTK	200
At-DBF2	EVCALKILNKKLGFKLNGTCHVLTERRSLTTTTRSETNVKLLSGTTPVSGRGMATESELGGDFRTESIGRRCLCKSGHARFYISEMFCVAVNEKHLLSKT...	287
DBF2	EVCALKILNKKLGFKLNETKHVLTERRDILTTTTRSENLVKLLYAFQDLQSLYLAMEFVPGGDFRLLINTRCLCKSGHARFYISEMFCVAVNALHDLGYTHRD	300
At-DBF2	.....DSTISNEEDSSINIRLEKFKDLGYPALSEKSIDRRKLY.....TCPNSMVGSPDYTALEVLGRKRYEYTVDYWS	356
DBF2	LKPENFLIDAKGHIKLTDFGLAAGTISNERIESMKTRLEKIDLEFPAPTEKSIDRRKMYNQLREKEINYANSVMGSPDYMALEVLGGKYDFTVDYWS	400
At-DBF2	LGCHLFESLVGYTPFSGSSTNETYATSRSWKOTLNRARHEDGRAAFYHRTWDLITRHRADLSTRTRSFHEVKMSYFADILFKALRSIIPFPPTQDSET	456
DBF2	LGCHLFESLVGYTPFSGSSTNETYDNLRRWJKTLLRRPRQSDGRAAFSDRTWDLITRLIADP INRLRSFENVRKMSYFADINFSTLRSMIPFPPTQDSET	500
At-DBF2	DAGYFDDFUNEADIAKYADVFNQCCRTALVDDSAVSSKLVGTFRRHNGKQSSGMLFNGLEHSDPFSTFY 528	
DBF2	DAGYFDDFTSEADMAKYADVFKRQDKLTAMVDDSAVSSKLVGTFRRHNGKQSSGMLFNGLEHSDPFSTFY 572	

FIGURE 1 A

2/15

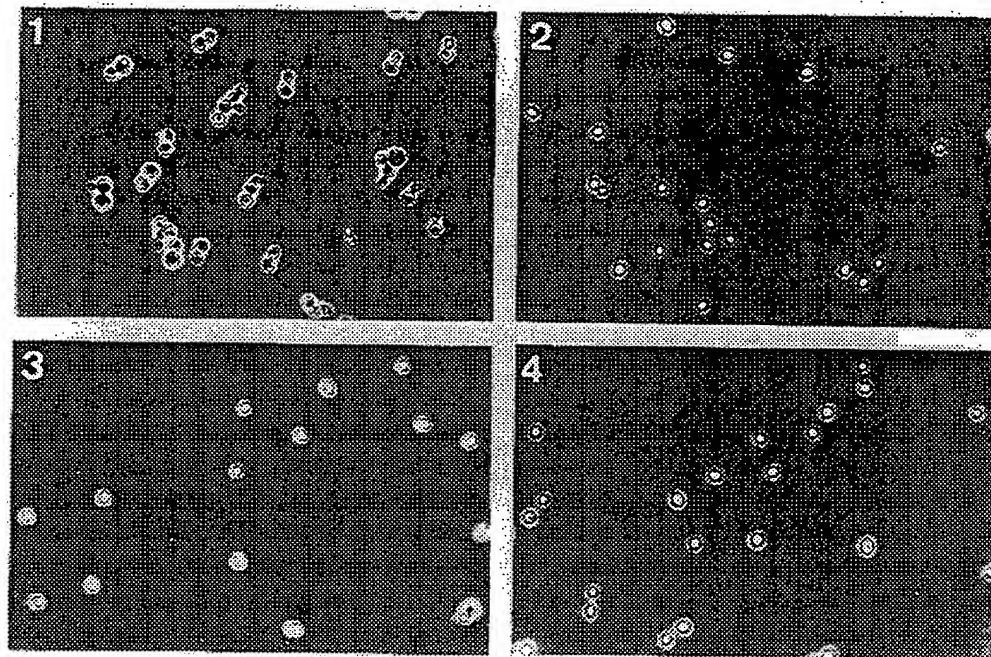


FIGURE 1B

3/15

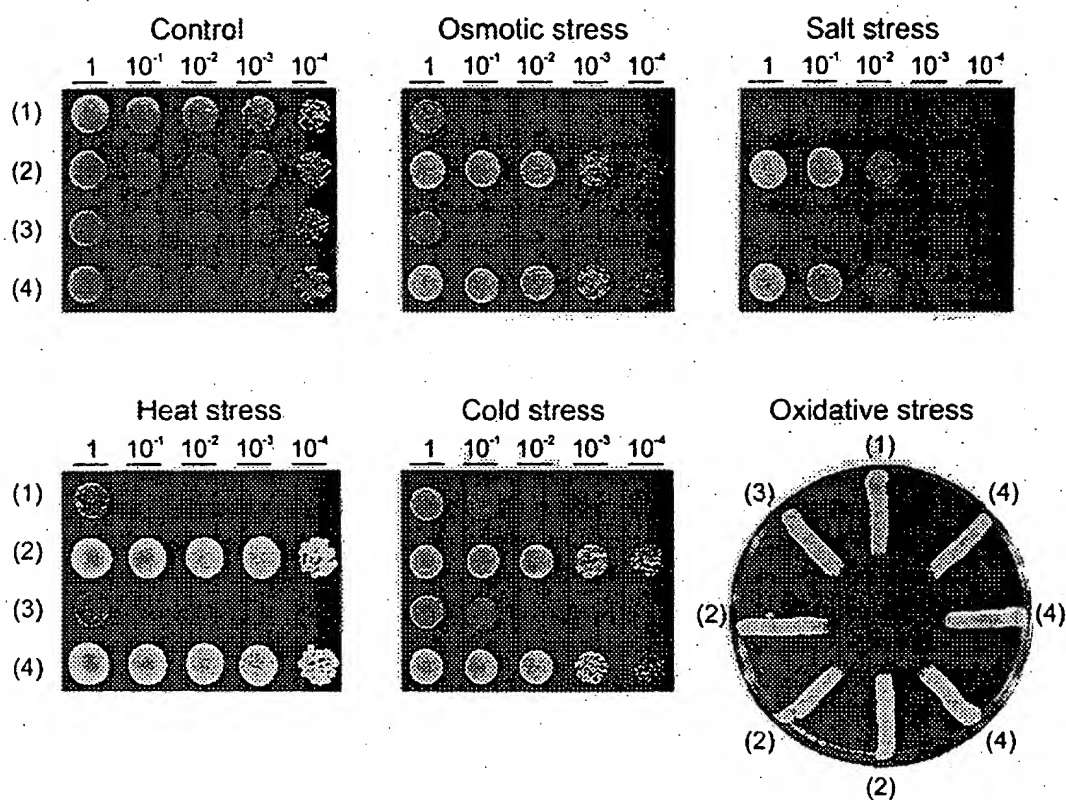


FIGURE 2

4/15

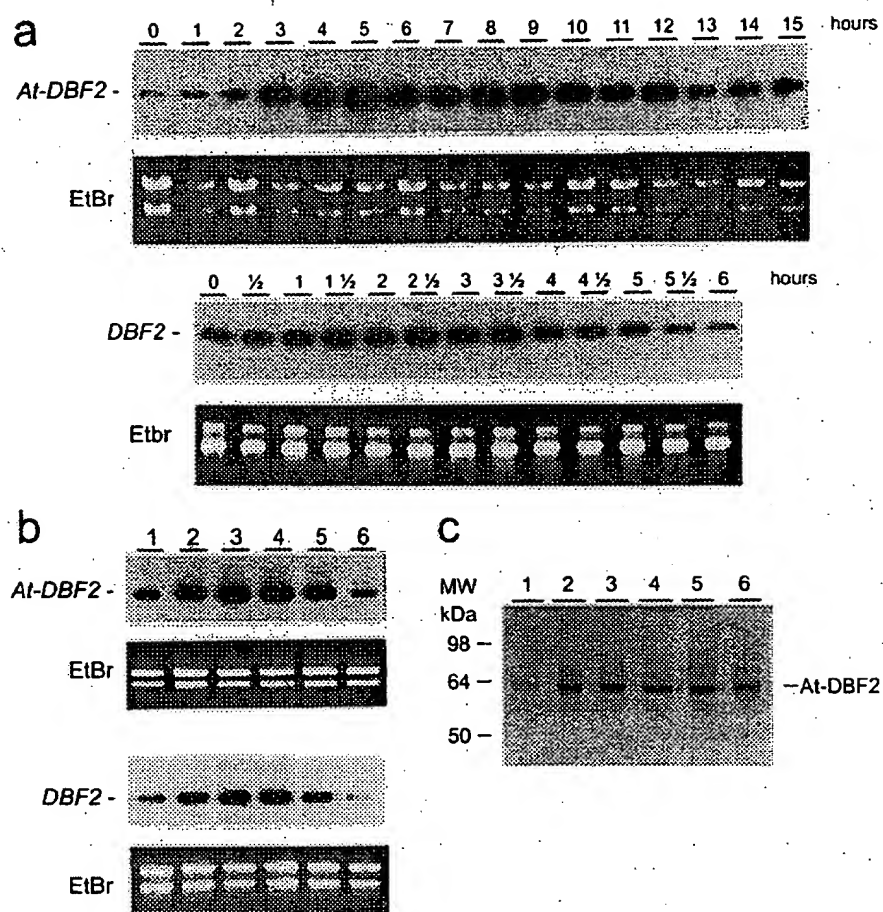


FIGURE 3



5/15

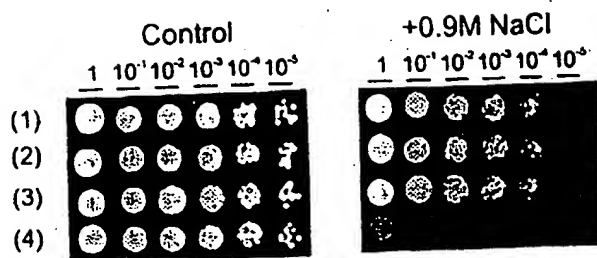


FIGURE 4

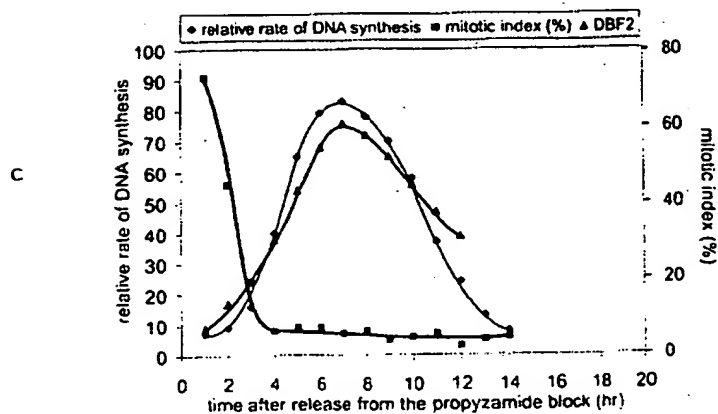
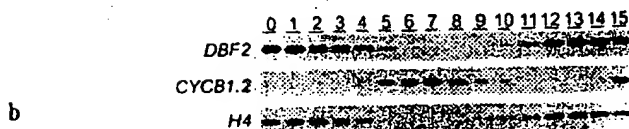
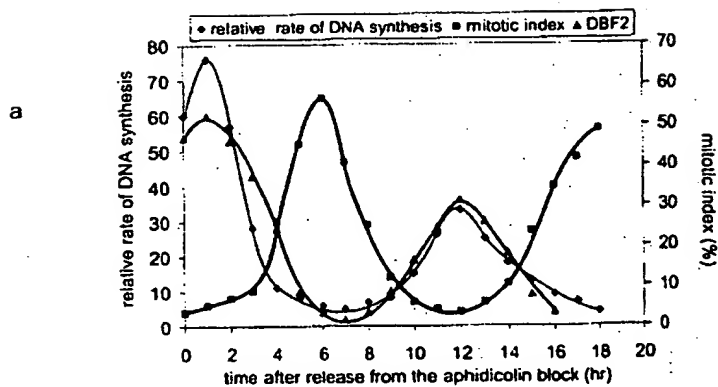


FIGURE 5

6/15

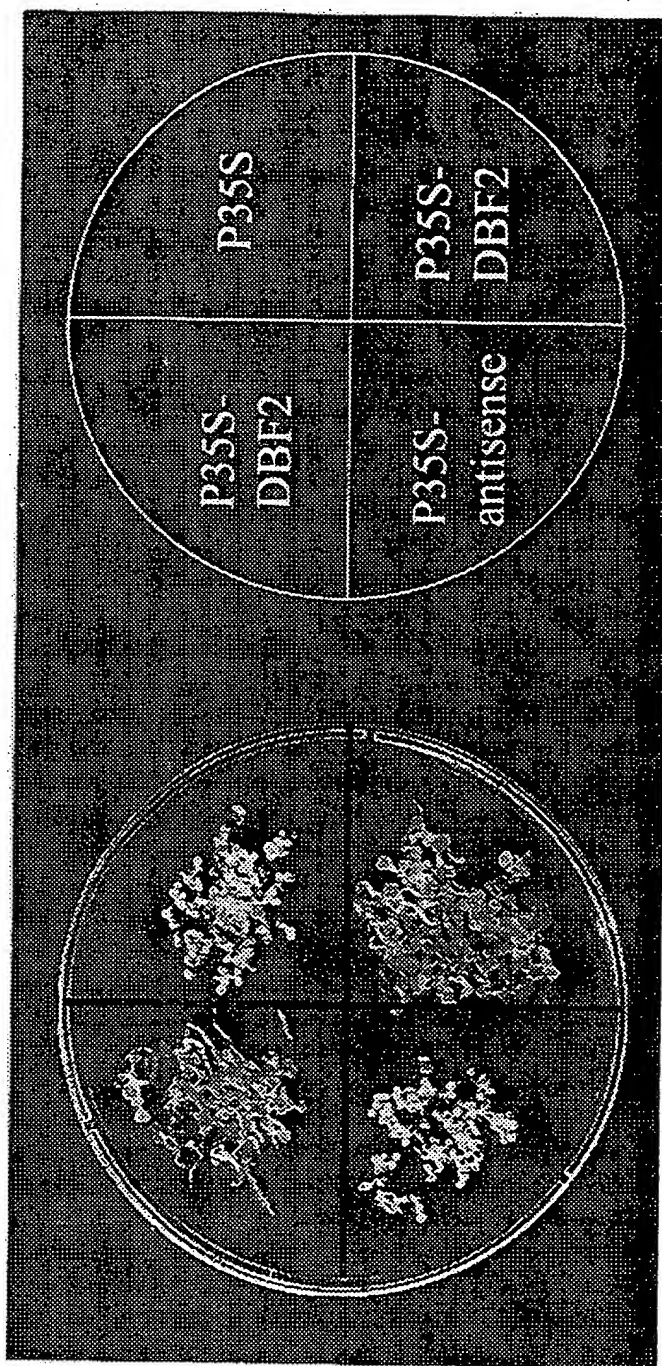


FIGURE 6

7/15

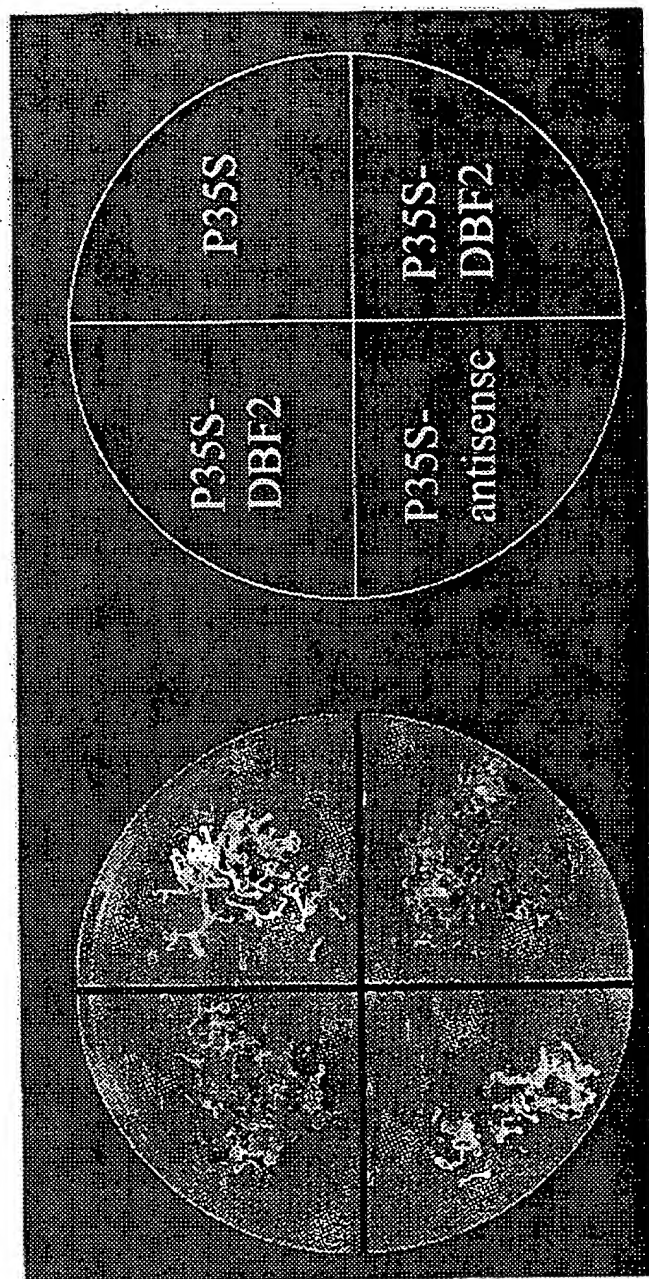


FIGURE 7

8/15

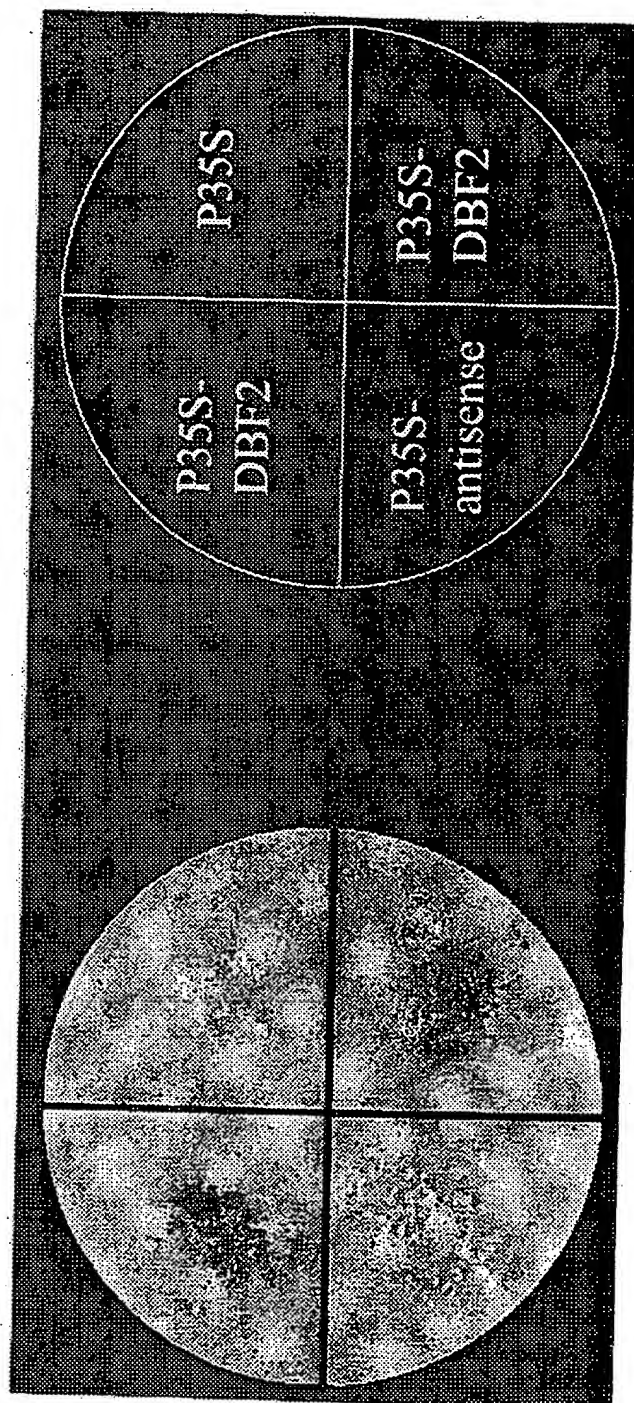


FIGURE 8

9/15

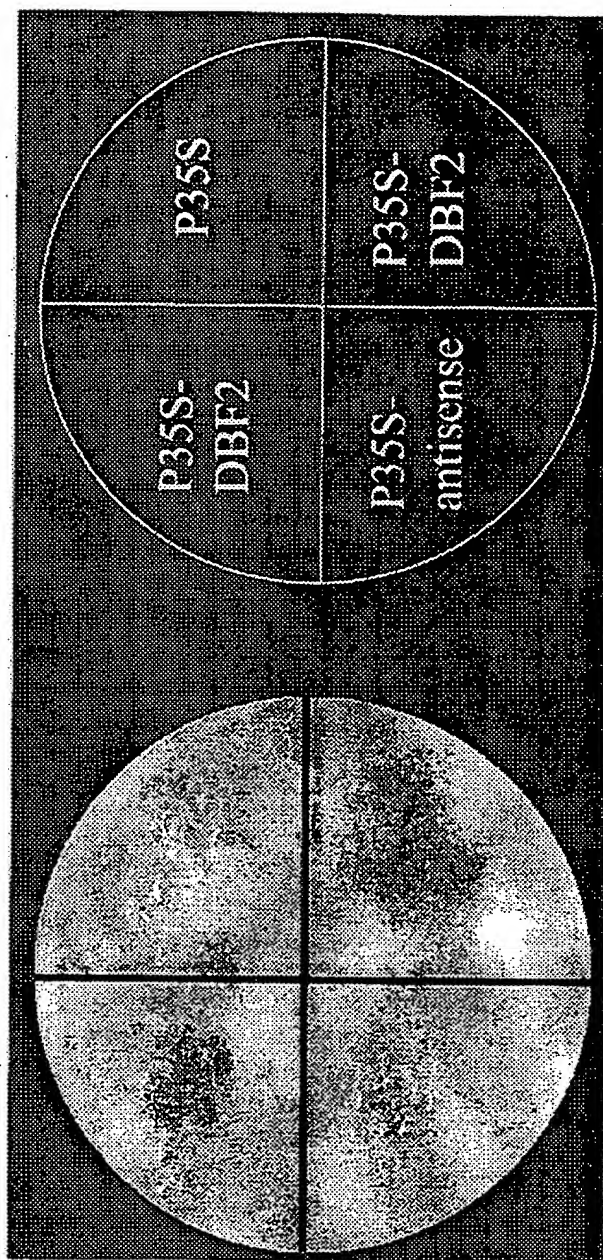


FIGURE 9

10/15

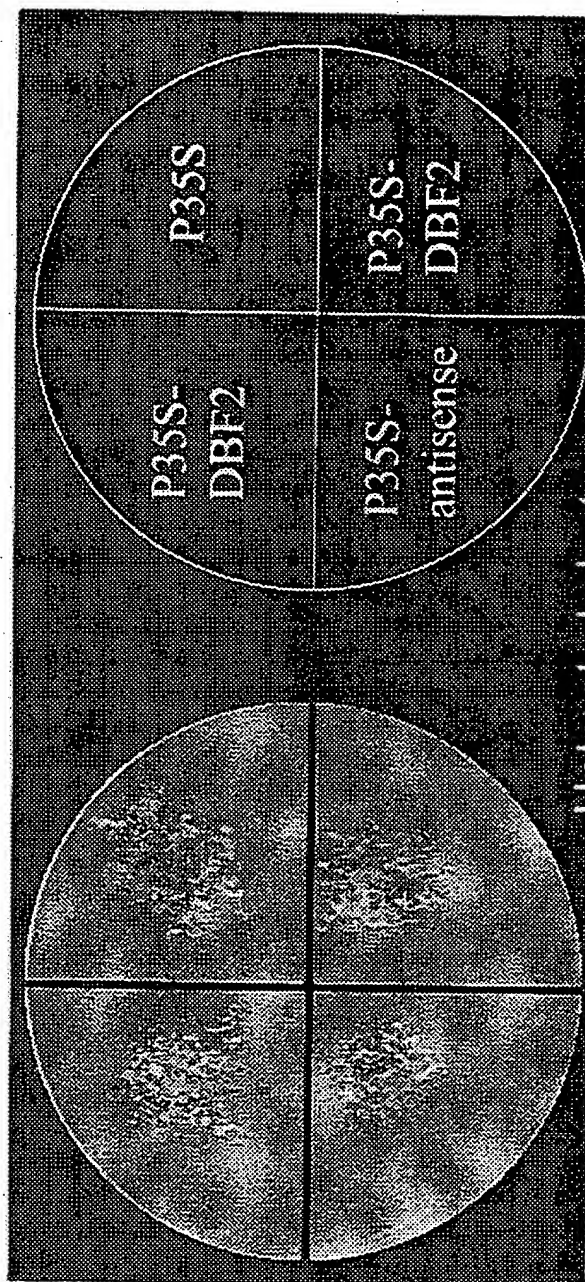


FIGURE 10

11/15

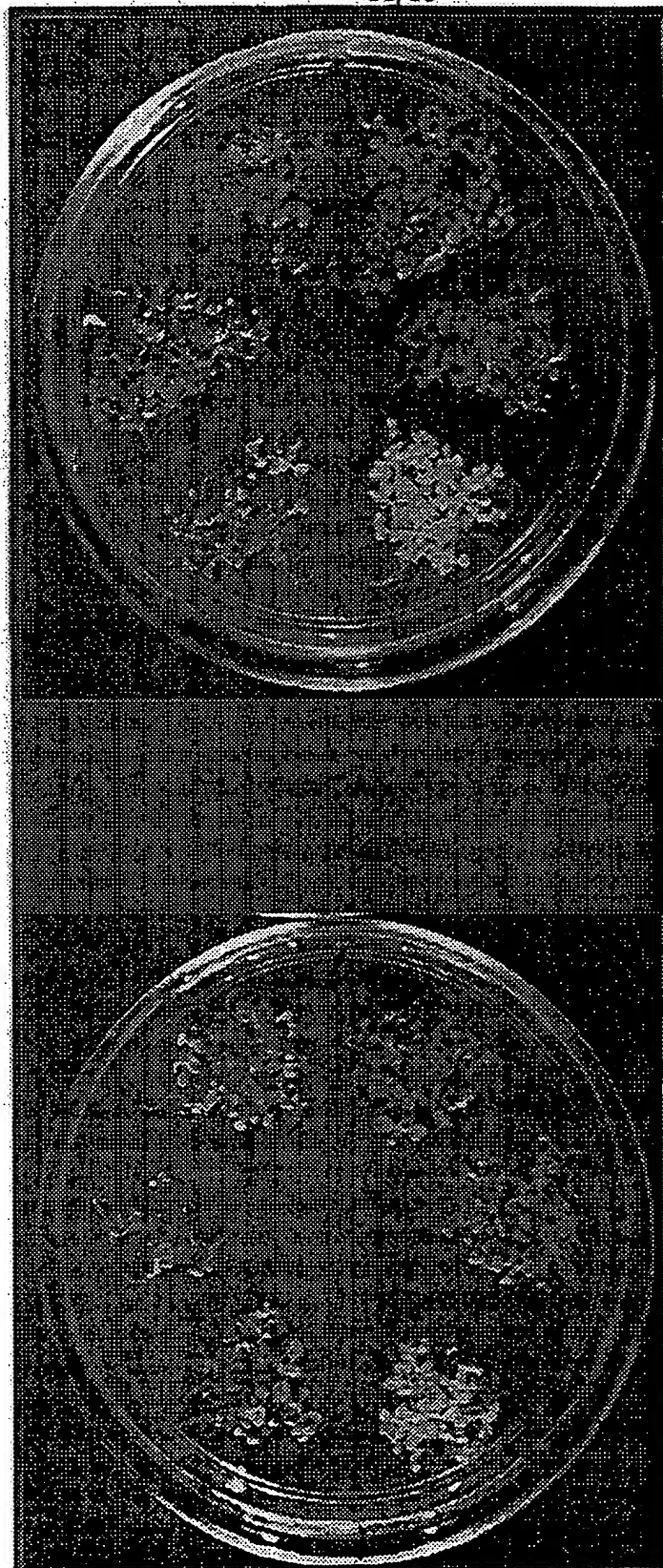


FIGURE 11



12/15



FIGURE 12A

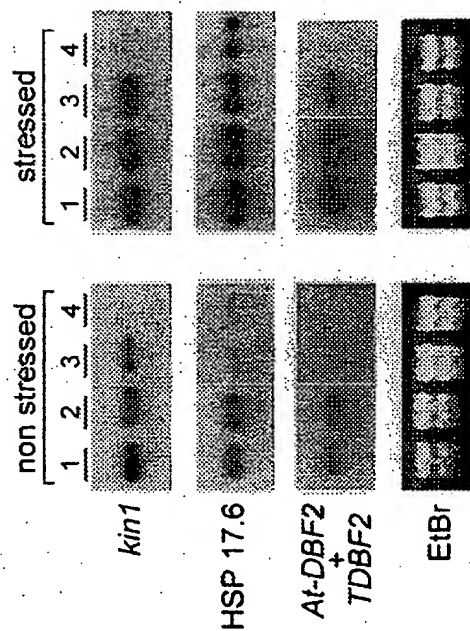


FIGURE 12c



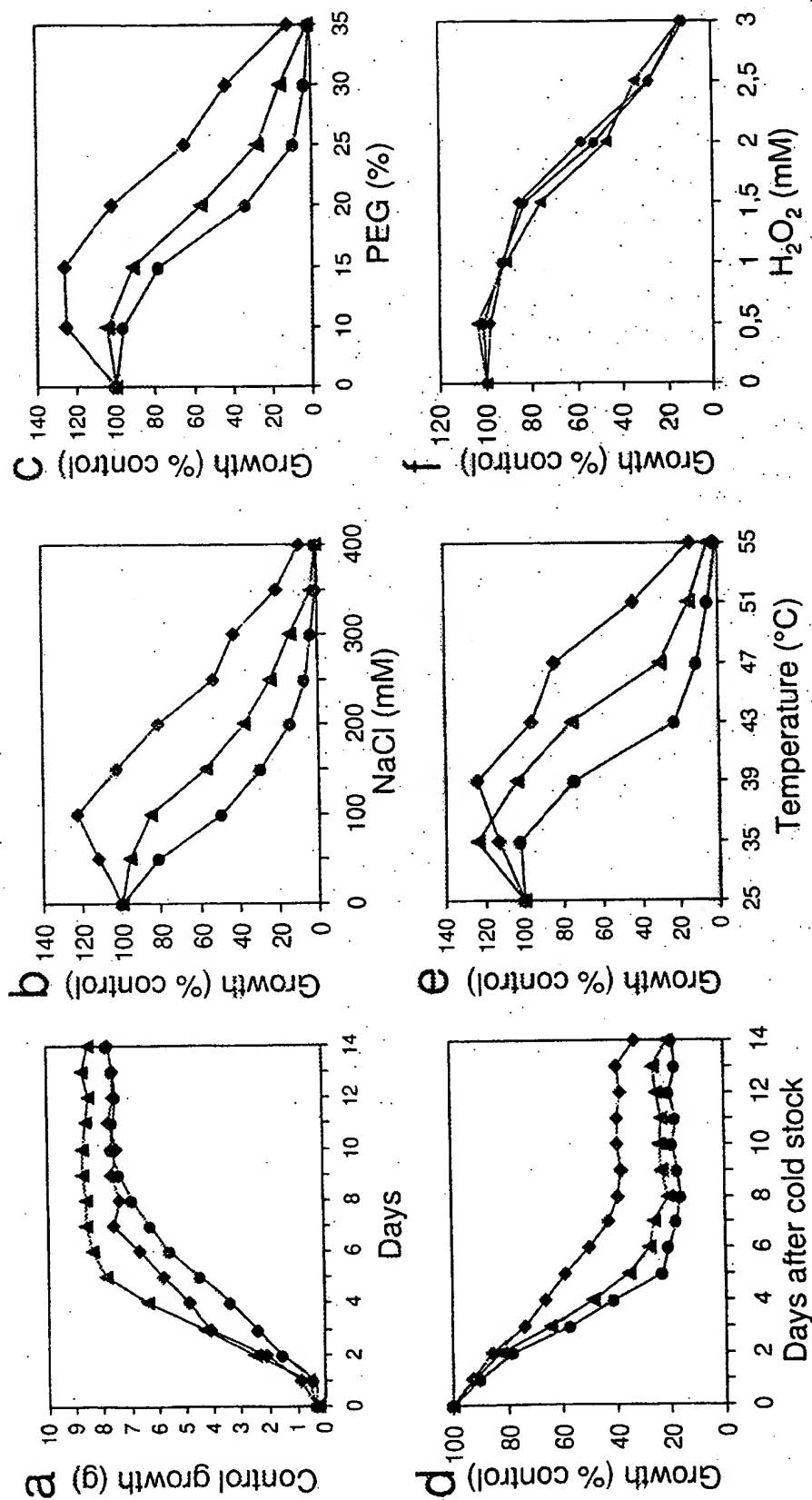


FIGURE 12B



FIGURE 13

15/15



FIGURE 14

## SEQUENCE LISTING

&lt;110&gt; VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE

&lt;120&gt; Genes involved in tolerance to environmental stress

&lt;130&gt; VIB-14-NV/OSMO

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 98202634.6

&lt;151&gt; 1998-08-04

&lt;160&gt; 126

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1909

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (40)..(1626)

&lt;400&gt; 1

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                                         Met Ala Gly Asn Met
                                         1      5

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Ser Cys Leu Ser Thr Asp Gly His Gly Thr Pro Gly Gly Ser Gly His
          10              15              20

ttc ccc aat cag aac cta acg aaa aga aga acg cgt cca gcg ggt atc      150
Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr Arg Pro Ala Gly Ile
          25              30              35

aac gac tcg cct tcg ccg gtg aaa tgc ttt ttt ttc ccc tat gaa gac      198
Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe Phe Pro Tyr Glu Asp
          40              45              50

acc tcc aac acg tca tta aag gaa gtg tcc cag ccc acg aaa tac agt      246
Thr Ser Asn Thr Ser Leu Lys Glu Val Ser Gln Pro Thr Lys Tyr Ser
          55              60              65

tcc aat tcc cct cca gtc agc ccg gca att ttt tat gag agg gcg acg      294
Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
          70              75              80              85

tcg tgg tgc acg caa agg gtg gtg agt ggg agg gca atg tac ttt cta      342
Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg Ala Met Tyr Phe Leu
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Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Ser Gln Leu Pro Asn	
120 125 130	
tct gac cag atc aag ctc aac gaa gag tgg tcc tcc tat tta cag aga	486
Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser Ser Tyr Leu Gln Arg	
135 140 145	
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Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys Pro Lys Asn Arg Asp	
150 155 160 165	
ttt gaa atg att aca caa gta ggt caa ggt ggt tat ggg cat gtt tat	582
Phe Glu Met Ile Thr Gln Val Gly Gln Gly Tyr Gly His Val Tyr	
170 175 180	
tta gcc aga aag aaa gac aca aaa gag gtg tgc gcc tta aaa att ttg	630
Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys Ala Leu Lys Ile Leu	
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Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr Cys His Val Leu Thr	
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Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu Thr Met Val Lys Leu	
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Leu Ser Gly Thr Thr Pro Val Gly Ser Arg Gly Met Ala Ile Glu Ser	
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250 255 260	
aaa agt ggc cat gcg aga ttc tat att agc gaa atg ttc tgt gcc gtc	870
Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu Met Phe Cys Ala Val	
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Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser Thr Ile Ser Asn Glu	
280 285 290	
gaa gat agt agc atc aac ata agg tta gaa aaa ttc aaa gac ctt ggg	966
Glu Asp Ser Ser Ile Asn Ile Arg Leu Glu Lys Phe Lys Asp Leu Gly	
295 300 305	
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Tyr Pro Ala Leu Ser Glu Lys Ser Ile Glu Asp Arg Arg Lys Leu Tyr	
310 315 320 325	
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Thr Cys Pro Asn Ser Met Val Gly Ser Pro Asp Tyr Ile Ala Leu Glu	

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agc gag acc gat gcc ggt tat ttc gat gac ttt tgg aat gag gct gac Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe Trp Asn Glu Ala Asp 455 460 465			1446
ata gcc aaa tac gct gac gtc ttt aat agt cag tgc tgc cgt acg gct Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln Cys Cys Arg Thr Ala 470 475 480 485			1494
tta gtc gac gat tct gct gtt tct tct aaa ctt gtt ggg ttc acc ttc Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu Val Gly Phe Thr Phe 490 495 500			1542
cga cac aga aat ggt aaa cag ggt tcc agt ggt atg tta ttc aac ggg Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly Met Leu Phe Asn Gly 505 510 515			1590
cta gaa cac tca gac ccc ttc tca acc ttt tac tag taatcggcag Leu Glu His Ser Asp Pro Phe Ser Thr Phe Tyr 520 525			1636
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gagctcgcca gctgcccag cctttcgccc cagcctgcca gccttttttt aaacgtgaa			1816
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1909

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35 40 45

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50 55 60

Pro Thr Lys Tyr Ser Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe  
65 70 75 80

Tyr Glu Arg Ala Thr Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg  
85 90 95

Ala Met Tyr Phe Leu Glu Tyr Tyr Cys Asp Met Phe Asp Tyr Val Ile  
100 105 110

Ser Arg Arg Gln Arg Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Gln  
115 120 125

Ser Gln Leu Pro Asn Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser  
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Ser Tyr Leu Gln Arg Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys  
145 150 155 160

Pro Lys Asn Arg Asp Phe Glu Met Ile Thr Gln Val Gly Gln Gly Gly  
165 170 175

Tyr Gly His Val Tyr Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys  
180 185 190

Ala Leu Lys Ile Leu Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr  
195 200 205

Cys His Val Leu Thr Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu  
210 215 220

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 260 265 270  
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 420 425 430  
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 465 470 475 480  
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu  
 485 490 495  
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Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu  
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Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp  
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Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp  
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gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306  
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile  
60 65 70

cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354  
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg  
75 80 85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402  
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu  
90 95 100

agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450  
Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala  
105 110 115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498  
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val  
120 125 130 135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546  
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile  
140 145 150

caa gtt caa gtc gct tga gttgtgtgt gatccgtgtt tttgtgtttt 594  
Gln Val Gln Val Ala  
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 Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val  
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                   85                  90                  95  
 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys  
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 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys  
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 Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu  
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Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr	
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aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt	267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu	
30 35 40 45	
cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat	315
Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn	
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cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat	363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp	
65 70 75	
cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc	411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg	
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Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe	
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Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg	
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Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala	
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Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn	
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Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys	
175 180 185	
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Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly	
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Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser	
210 215 220	
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Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser	
225 230 235	
cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc	891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly  
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 Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg  
 65 70 75 80  
 Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile  
 85 90 95  
 Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe  
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 Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe  
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Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val  
130 135 140

Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp  
145 150 155 160

Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile  
165 170 175

Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys  
180 185 190

Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu  
195 200 205

Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile  
210 215 220

His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met  
225 230 235 240

Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys  
245 250 255

Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp  
260 265 270

Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu  
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Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala  
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Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
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Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
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His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
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Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg	483
Cys Thr Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
140 145 150 155	
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Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat	579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
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Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
190 195 200	
aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa	675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys	
205 210 215	
ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa	723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln	
220 225 230 235	
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Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly	
240 245 250	
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His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met  
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Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys  
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Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser  
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Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala  
 115 120 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser  
 130 135 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys  
 145 150 155 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser  
 165 170 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp  
 180 185 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn  
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Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr  
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Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

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 Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe  
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 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr  
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gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808  
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val  
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Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
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Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365	
ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc				2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca				2384
Met His Arg Asp Glu Glu	385			
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			Ile	
			390	
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Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val	395	400	405	
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Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
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Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
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Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
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ctaaaaacatt atttatctct ctgtatctct cag gct gat cga tcc ttg gga cag				2904
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Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

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 Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys Ala Asp Arg Ser Leu Gly  
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Asn	Leu	Gly	Thr	Ile	Ala	Arg	Ser	Gly	Thr	Lys	Glu	Phe	Met	Glu	Ala				
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ctt	caa	gct	gga	gct	gat	gta	agc	atg	ata	gga	caa	ttt	ggg	gtt	ggg	852			
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cac	aat	gat	gat	gaa	caa	tac	gtt	tgg	gag	tct	caa	gct	ggg	ggg	tcc	948			
His	Asn	Asp	Asp	Glu	Gln	Tyr	Val	Trp	Glu	Ser	Gln	Ala	Gly	Gly	Ser				
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aag	atc	agc	ctc	ttc	ctt	aag	gac	gat	cag	gtaaggaatc	gtagctttga					1046			
Lys	Ile	Ser	Leu	Phe	Leu	Lys	Asp	Asp	Gln										
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Lys	His	Ser	Glu	Phe	Ile	Ser	Tyr	Pro	Ile	Tyr	Leu	Trp	Thr	Glu	Lys				
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acc	acc	gag	aag	gag	atc	agt	gac	gat	gag	gat	gaa	gat	gaa	cca	aag	1251			
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Ile Asp Ala Gln Leu Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp  
15 20 25

gat aag ctt gtt gag tac gat gct ctt ctc ctt gat cgc ttt ctc gac 146  
Asp Lys Leu Val Glu Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp  
30 35 40

att ctc cag gat tta cac ggc gag gat ctc cgt gaa acg gtt caa gag 194  
Ile Leu Gln Asp Leu His Gly Glu Asp Leu Arg Glu Thr Val Gln Glu  
45 50 55

tta tac gag ctt tct gct gag tat gaa ggg aag cgt gag cct agc aag 242  
Leu Tyr Glu Leu Ser Ala Glu Tyr Glu Gly Lys Arg Glu Pro Ser Lys  
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Leu Glu Glu Leu Gly Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser  
80 85 90

att gtt atc tcc aag gct ttc tct cac atg ctt aac tta gcc aat ttg 338  
Ile Val Ile Ser Lys Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu  
95 100 105

gct gag gag gtg cag att gct cac cgt cgc agg atc aag aag ctg aag 386  
Ala Glu Glu Val Gln Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys

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Lys Gly Asp Phe Val Asp Glu Ser Ser Ala Thr Thr Glu Ser Asp Ile			
125	130	135	
gaa gag act ttt aag agg ctc gtt tgc gat ctt ggt aag tct cct gaa			482
Glu Glu Thr Phe Lys Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu			
140	145	150	155
gag atc ttt gat gcc ttg aag aat cag act gtg gat ctg gtt ttg act			530
Glu Ile Phe Asp Ala Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr			
160	165	170	
gct cat cct act cag tct gtg cgt aga tca ttg ctt cag aag cat ggg			578
Ala His Pro Thr Gln Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly			
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agg ata agg gac tgt ctt gct caa ctc tat gca aag gac att act cct			626
Arg Ile Arg Asp Cys Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro			
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Asp Asp Lys Gln Glu Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala			
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Ala Phe Arg Thr Asp Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp			
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gaa atg aga gct gga atg agt tat ttc cac gag aca atc tgg aaa ggt			770
Glu Met Arg Ala Gly Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly			
240	245	250	
gtc ccc aag ttc ttg cgc cgt gtg gac aca gct ctg aaa aac att ggg			818
Val Pro Lys Phe Leu Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly			
255	260	265	
att gat gaa cgt gtt cct tac aat gcc cca ttg att caa ttc tct tgc			866
Ile Asp Glu Arg Val Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser			
270	275	280	
tgg atg ggc ggt gat cgt gat ggt aat ccg agg gtc aca cct gag gtc			914
Trp Met Gly Gly Asp Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val			
285	290	295	
act aga gat gtg tgc ttg ttg gct aga atg atg gct gcc aat ctc tac			962
Thr Arg Asp Val Cys Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr			
300	305	310	315
tat aac caa atc gag aat ctg atg ttt gag tta tct atg tgg cgt tgc			1010
Tyr Asn Gln Ile Glu Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys			
320	325	330	
act gat gaa ttc cgt gtg cgg gcg gat gaa ctg cac agg aac tca agg			1058
Thr Asp Glu Phe Arg Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg			
335	340	345	

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act gag cca tac cgt gtg att ctt ggt gat gtg agg gat aag ctg tat	1154
Thr Glu Pro Tyr Arg Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr	
365 370 375	
cac aca cgt gag cgt tcc cgc caa ttg ctg agt aat gga atc tcg gat	1202
His Thr Arg Glu Arg Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp	
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Ile Pro Glu Glu Ala Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro	
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415 420 425	
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Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly	
430 435 440	
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Leu Ser Leu Val Arg Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr	
445 450 455	
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Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
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Arg Asp Trp Ser Glu Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu	
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Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
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Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp	
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Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro	
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Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
560 565 570	

cct gcc gct gtt gca aga ctc ttt tct ata gac tgg tac aaa aac cgt	1778
Pro Ala Ala Val Ala Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg	
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Ile Asn Gly Lys Gln Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys	
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Asp Ala Gly Arg Leu Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu	
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Glu Leu Val Lys Val Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe	
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His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu	
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Ala Ile Leu Ser Gln Pro Pro Asp Thr Val Asn Gly Ser Leu Arg Val	
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Thr Val Gln Gly Glu Val Ile Glu Gln Ser Phe Gly Glu Ala His Leu	
670 675 680	
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Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly	
685 690 695	
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Glu Met Ala Val Val Ala Thr Glu Glu Tyr Arg Ser Val Val Phe Gln	
720 725 730	
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735 740 745	
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Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro Ser	
750 755 760	
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Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr	
765 770 775	
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Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe	
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Arg Tyr Ala Ile Lys Lys Asp Val Arg Asn Leu His Met Leu Gln Asp	
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Met Tyr Lys Gln Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Ile Glu	
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Leu Leu Val Ser Glu Asp Leu Trp Ala Phe Gly Glu Lys Leu Arg Ala	
845 850 855	
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Asn Phe Asp Glu Thr Lys Asn Leu Val Leu Gln Thr Ala Gly His Lys	
860 865 870 875	
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880 885 890	
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Asp Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys	
895 900 905	
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Arg Ile Arg Asp Ala Asn Tyr Asn Val Thr Leu Arg Pro His Ile Ser	
910 915 920	
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Lys Glu Ile Met Gln Ser Ser Lys Ser Ala Gln Glu Leu Val Lys Leu	
925 930 935	
aac ccc acg agt gaa tac gcg cct gga ctt gag gac aca ctt atc tta	2882
Asn Pro Thr Ser Glu Tyr Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu	
940 945 950 955	
acc atg aag ggt att gct gca gga ttg caa aac acc ggt taa gtgagtc	2932
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20 25 30

Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp Leu
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Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu Glu Val Gln		
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Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys Lys Gly Asp Phe Val		
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Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr Ala His Pro Thr Gln		
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Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly Arg Ile Arg Asp Cys		
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Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro Asp Asp Lys Gln Glu		
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Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala Ala Phe Arg Thr Asp		
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Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp Glu Met Arg Ala Gly		
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Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly Ile Asp Glu Arg Val		
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Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser Trp Met Gly Gly Asp		
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Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val Thr Arg Asp Val Cys		
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Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr Tyr Asn Gln Ile Glu		
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Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys Thr Asp Glu Phe Arg		
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Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg Lys Asp Ala Ala Lys		

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Thr	Phe	Thr	Asn	Val	Glu	Gln	Phe	Leu	Glu	Pro	Leu	Glu	Leu	Cys	Tyr				
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Pro	Phe	Phe	Arg	Val	Thr	Ile	Asp	Leu	Ile	Glu	Met	Val	Phe	Ala	Lys
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Gly Ser Ala Val Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp  
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45                                      50                                      55                                      60

cct ccc gtc gtc atg aac cct atc agt cgc cag aat ttc atc gtc aag 244  
Pro Pro Val Val Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys  
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Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp Gly Ala Ala Thr  
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 Ile Ala Asn Lys Asn Cys Ala Pro Ile Met Leu Arg Leu Ala  
 25 30 35

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 aaatgtttgt atcatctggt ttttatgaag a tgg cac gat gct gga acc tat 315  
 Trp His Asp Ala Gly Thr Tyr  
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gat gct caa tcg aag acc ggt gga cct aat ggc tct atc agg aac gaa 363  
 Asp Ala Gln Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu  
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gaa gag cac act cat ggt gcc aac agt ggt ttg aag atc gct ctc gat 411  
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 Glu  
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Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His  
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Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu  
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Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys  
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Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe  
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Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile  
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Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr  
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 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu  
 245 250 255  
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp  
 260 265 270  
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser  
 275 280 285  
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile  
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 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg  
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 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe  
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 Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly  
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 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194  
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys  
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Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
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Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
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Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
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Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
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Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
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Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
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cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
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Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
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gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
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255 260 265 270	
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Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
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 ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055  
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 Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly  
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 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val  
 145 150 155 160  
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Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp  
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 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly  
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 260 265 270  
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 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly  
 35 40 45

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Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met	
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Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg	
65 70 75	
gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga	287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg	
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Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu	
100 105 110	
aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc	383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr	
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Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg	
130 135 140	
aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac	479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn	
145 150 155	
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Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys	
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Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys	
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Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser	
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Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln	
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Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser	
225 230 235	
tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca	768
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 Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg  
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 Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn  
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 Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp  
 115 120 125  
 His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys  
 130 135 140  
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 145 150 155 160  
 Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala  
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 Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg  
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 Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp  
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 Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg  
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 Thr Glu Lys Ala Phe Leu Lys  
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cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217  
 Gln Pro Lys Val Phe Leu Se  
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tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

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 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
 35 40 45

gcc att gat g gtatgtttta gcttttaact cgttataata gataaggaac 423  
 Ala Ile Asp G  
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tcttggttg ttgtgttcat atagtcgata gatttcaaat gctattttgt cttgtagaat 483

cttaagcttt ggtttagtga gttctgattc ttcagcttta tctggatcta cattactgtt 543

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 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu  
 370 375 380  
 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly  
 385 390 395 400



Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp  
 405 410 415  
 Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr  
 420 425 430  
 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp  
 435 440 445  
 Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met Lys Ser Lys Ser Asn  
 450 455 460  
 Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr Gly Val Pro Cys Asp  
 465 470 475 480  
 Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp  
 485 490 495  
 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys  
 500 505 510  
 Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu Leu Glu Glu Phe His  
 515 520 525  
 Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala Leu Gly Asp Thr Asn  
 530 535 540  
 Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser Lys Thr Pro Lys Arg  
 545 550 555 560  
 Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp Ala Met Pro Ser Pro  
 565 570 575  
 Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser Arg Val Met Gln Ser  
 580 585 590  
 Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn  
 595 600 605  
 Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu  
 610 615 620  
 Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala  
 625 630 635 640  
 Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly  
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ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg	96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp	
20 25 30	
agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct	144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro	
35 40 45	
cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala	
50 55 60	
ccc cct cct cgt cag cct cca cgt cct cca aca gca cgg tgg tca gcg	240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala	
65 70 75 80	
atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg cgg agt aga	288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg	
85 90 95	
cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg	336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp	
100 105 110	
cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
115 120 125	
ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg	432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg	528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
165 170 175	
aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser 225 230 235 240			720
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile 245 250 255			768
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr 260 265 270			816
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val 275 280 285			864
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu 290 295 300			912
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly 305 310 315 320			960
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggc Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly 325 330 335			1008
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggc gca Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala 340 345 350			1056
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile 355 360 365			1104
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala 370 375 380			1152
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn 385 390 395 400			1200
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg 405 410 415			1248
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr 420 425 430			1296
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr 435 440 445			1344

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
 500 505 510  
 ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584  
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr  
 515 520 525  
 gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635  
 Gly Arg Arg Trp Arg Glu  
 530 535  
 tggaccgggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695  
 taaaaaaaaac caacaaaaaaaa aaaaaaaaaaac aaaaaaaaaa a 1736

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&lt;211&gt; 534

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 36

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 20 25 30  
 Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro  
 35 40 45  
 Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala  
 50 55 60  
 Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala  
 65 70 75 80  
 Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg  
 85 90 95  
 Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp  
 100 105 110

Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln  
 115 120 125  
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met  
 130 135 140  
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg  
 145 150 155 160  
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala  
 165 170 175  
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val  
 180 185 190  
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn  
 195 200 205  
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly  
 210 215 220  
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser  
 225 230 235 240  
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile  
 245 250 255  
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr  
 260 265 270  
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val  
 275 280 285  
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu  
 290 295 300  
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly  
 305 310 315 320  
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly  
 325 330 335  
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala  
 340 345 350  
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile  
 355 360 365  
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala  
 370 375 380  
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn  
 385 390 395 400  
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg  
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr  
 420 425 430  
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr  
 435 440 445  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
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 515 520 525  
 Gly Arg Arg Trp Arg Glu  
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<210> 37  
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 1 5 10  
 gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg 97  
 Ala Lys Lys Gly Ala Asn Leu Phe Lys  
 15 20  
 ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca cttttag 155  
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203  
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys  
 25 30 35

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att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
      40              45              50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
      55              60              65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
Lys Asp Asp Thr Leu
      70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
      Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
              75              80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
      85              90              95              100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503
Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
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acccc 508

<210> 38
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<213> Arabidopsis thaliana

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Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
      35              40              45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
      50              55              60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
      65              70              75              80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
      85              90              95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
      100              105              110

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tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96  
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys  
 20 25 30

acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144  
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro  
 35 40 45



gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192  
 Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys  
 50 55 60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240  
 Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val  
 65 70 75 80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288  
 Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe  
 85 90 95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336  
 Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu  
 100 105 110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384  
 Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr  
 115 120 125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432  
 Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys  
 130 135 140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480  
 Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser  
 145 150 155 160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528  
 Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr  
 165 170 175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576  
 Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu  
 180 185 190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtttc ttgattgata 629  
 Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys  
 195 200

actttagtat acattgaatt ggctttaaaag gtgtgtactt tggtgttttg ttacag gtg 688  
 Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736  
 Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser  
 205 210 215 220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784  
 Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys  
 225 230 235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832  
 Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser  
 240 245 250

cac tgc att gtaagaacga tcttcttgat tgatgtgat gcatagcttt 881

His Cys Ile  
255

atgcagctta tctctgtttt aacttactag tgtggttggt tctttttgta g atc ata 938  
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986  
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala  
260 265 270

ggc tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034  
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys  
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090  
Met Gln  
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144  
Thr Ala Lys Ile Asn  
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192  
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly  
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240  
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln  
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtggt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355  
Asp Ser Phe Glu Asp  
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403  
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys  
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451  
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys  
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499  
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly  
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547  
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met  
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595  
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys  
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
aac tgc ttc aac ggt gca gat gac aag gaa tca gcc tcg tct aga agg	2315
Asn Cys Phe Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg	

640	645	650	
ttg aga att caa aac att ttc acc ctt tgt ggc aat cag aga gag ctg			2363
Leu Arg Ile Gln Asn Ile Phe Thr Leu Cys Gly Asn Gln Arg Glu Leu			
655	660	665	
tct caa cac agt gga cag gag gag gat caa gcc aat att gca tca cct			2411
Ser Gln His Ser Gly Gln Glu Glu Asp Gln Ala Asn Ile Ala Ser Pro			
670	675	680	685
gat aag aaa gac aat cag ttc ttt tct att acg aat aag gcc gaa gca			2459
Asp Lys Lys Asp Asn Gln Phe Phe Ser Ile Thr Asn Lys Ala Glu Ala			
	690	695	700
cta gca gta gaa gaa gca aag gaa aac aat atc tca gtc gat caa agg			2507
Leu Ala Val Glu Glu Ala Lys Glu Asn Asn Ile Ser Val Asp Gln Arg			
	705	710	715
gaa aac ggt cag cta gat atc tat gtt aaa tgg gaa aca gct gct gat			2555
Glu Asn Gly Gln Leu Asp Ile Tyr Val Lys Trp Glu Thr Ala Ala Asp			
	720	725	730
aac cct cga aag ctc ata aca aca ctg aga gtt aca aag gat gca aca			2603
Asn Pro Arg Lys Leu Ile Thr Thr Leu Arg Val Thr Lys Asp Ala Thr			
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acagagtcac ctgacaattt aaacgaagg agattcctag tgatcaaagc atcaccaatg 6464  
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<213> Arabidopsis thaliana
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Gly Lys Asp Gly Trp Val Pro Thr Pro Ser Glu Asp Tyr Ser His Trp
      35              40              45

Ser His Arg Asn Arg Phe Gln Val Asn Asp Thr Leu His Phe Lys Tyr
      50              55              60

Ala Lys Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn
      65              70              75              80

Thr Cys Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser
      85              90              95

Leu Phe Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn
      100              105              110

Ser Gln Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser
      115              120              125

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Thr Val His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser  
 130 135 140  
 Pro Val His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu  
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 Pro Ser Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr  
 165 170 175  
 Ala Pro Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu Val  
 180 185 190  
 Val Asn Ser Ile Ile Lys Pro Ile Asp Ser Phe Leu Leu Lys Ser Leu  
 195 200 205  
 Pro Leu Val Val Asp Val Ala Val Gly Ile Ser Thr Ser Arg Gln Leu  
 210 215 220  
 Gln Ala Ser Glu Glu Pro Val Ser Ser Pro Leu Ser Ser Pro Ala Leu  
 225 230 235 240  
 Leu Gly Ser Gly Lys Glu Glu Glu Gln Lys Ile Ile Pro Lys Arg Gln  
 245 250 255  
 Lys Val Gln Ala Val Leu Lys Ser Ile Lys Gln Ser Pro Lys Lys Val  
 260 265 270  
 Asn Leu Val Ala Ala Leu Val Arg Gly Met Arg Val Glu Asp Ala Leu  
 275 280 285  
 Ile Gln Leu Gln Val Thr Val Lys Arg Ala Ala Gln Thr Val Tyr Arg  
 290 295 300  
 Val Ile His Ala Ala Arg Ala Asn Ala Thr His Asn His Gly Leu Asp  
 305 310 315 320  
 Pro Asp Arg Leu Leu Val Ala Glu Ala Phe Val Gly Lys Gly Leu Phe  
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 Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile Ser  
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 Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro Glu  
 355 360 365  
 Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys Lys  
 370 375 380  
 Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr Ser  
 385 390 395 400  
 Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser Glu  
 405 410 415  
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 420 425 430

Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His  
 435 440 445

Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile  
 450 455 460

Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val  
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Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg  
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 Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser  
 10 15 20 25

ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148  
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro  
 30 35 40

gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196  
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys  
 45 50 55

tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct 244  
 Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser  
 60 65 70

tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca 292  
 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser  
 75 80 85

acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct 340  
 Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser  
 90 95 100 105

tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac 388



Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala  
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 Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met  
 115 120 125  
 Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala  
 130 135 140  
 Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val  
 145 150 155 160  
 Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg  
 165 170 175  
 Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val  
 180 185 190  
 His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp  
 195 200 205  
 Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys  
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 Ala Ile Glu Glu Glu Ala  
 225 230

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 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <222> (12)..(1193)

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 cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98  
 Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro  
 15 20 25  
 agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146  
 Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys  
 30 35 40 45  
 tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194  
 Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr  
 50 55 60  
 cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp	
65 70 75	
ggt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt	290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser	
80 85 90	
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat	338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His	
95 100 105	
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta	386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val	
110 115 120 125	
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct	434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro	
130 135 140	
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct	482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala	
145 150 155	
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt	530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly	
160 165 170	
ggt ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat	578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His	
175 180 185	
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc	626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala	
190 195 200 205	
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag	674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu	
210 215 220	
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt	722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val	
225 230 235	
ggt tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct	770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala	
240 245 250	
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg	818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met	
255 260 265	
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat	866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His	
270 275 280 285	
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata	914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile	

290	295	300	
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg			962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met			
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tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg			1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp			
320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct			1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro			
335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc			1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe			
350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga			1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly			
370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaaaa			1203
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<213> Arabidopsis thaliana			
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20	25	30	
Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile			
35	40	45	
Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val			
50	55	60	
Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly			
65	70	75	80
Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu			
85	90	95	
Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr			
100	105	110	
Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu			
115	120	125	

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln  
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 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile  
 145 150 155 160  
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser  
 165 170 175  
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu  
 180 185 190  
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His  
 195 200 205  
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys  
 210 215 220  
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val  
 225 230 235 240  
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val  
 245 250 255  
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro  
 260 265 270  
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu  
 275 280 285  
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val  
 290 295 300  
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg  
 305 310 315 320  
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu  
 325 330 335  
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala  
 340 345 350  
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe  
 355 360 365  
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn  
 370 375 380  
 Ser Tyr Thr Asp Glu Thr Asp His Thr  
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&lt;210&gt; 47

&lt;211&gt; 1194

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1194)

&lt;400&gt; 47

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cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg	96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	
20 25 30	
caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt	144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	
35 40 45	
aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt	192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	
50 55 60	
att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt	240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	
65 70 75 80	
tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc	288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	
85 90 95	
aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc	336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	
100 105 110	
act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc	384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	
115 120 125	
gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat	432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	
130 135 140	
aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct	480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	
145 150 155 160	
agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg	528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	
165 170 175	
acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca	576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	
180 185 190	
gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att	624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	
195 200 205	



cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672  
 Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys  
 210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720  
 Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu  
 225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768  
 Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala  
 245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816  
 Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg  
 260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864  
 Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu  
 275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912  
 Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu  
 290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960  
 Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser  
 305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008  
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr  
 325 330 335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056  
 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu  
 340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104  
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu  
 355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152  
 Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser  
 370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194  
 Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn  
 385 390 395

&lt;210&gt; 48

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

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Gln Asn Lys Asp	Gly Arg Ala	Leu Gln Lys Val	Leu Gly Thr Ile Arg
35		40	45
Asn Gly Asp Leu	Ala Val Ser	Ala Pro Lys Thr	Ser Leu Arg Ala Gly
50		55	60
Ile Phe Gly Glu	Gly Ser Ser	Leu Val Asp	Gln Met Pro Cys Lys Val
65		70	75
Tyr Val Ala Phe	His Lys Glu	Ser Tyr Cys	Ser Leu Thr Gly Leu Ser
	85	90	95
Lys Arg Gly Val	Ala Ile Asn	Glu Ala Ser	Leu Ser Leu Val Gly Ile
100		105	110
Thr Lys Val Arg	Ala Pro Val	Gly Asn Thr	Val Gly Ala Glu Ala Thr
115		120	125
Val Tyr Ile Gly	Ser Pro Lys	Pro Tyr Thr	Glu Cys Ser Thr Pro Asn
130		135	140
Lys Met Tyr Ala	Val Ala Ala	Gly Phe Lys	Val Ala Ser Phe Ala Ala
145		150	155
Ser Thr Cys Val	Arg Pro Pro	Ala Arg Ala	Arg Thr Leu Thr Val
	165	170	175
Thr Ser Thr Val	Thr Leu Ser	Met Ala Thr	Gly Lys Cys Val Asn Thr
180		185	190
Gly Asn Glu Pro	Val Ser Lys	Pro Thr Gly	Val Arg Met Met Leu Ile
195		200	205
Pro Leu Asp Ala	Thr Leu Ile	Lys Val Trp	Thr Gly Glu Val Lys Lys
210		215	220
Ala Ile Val Ser	Arg Pro Ala	Lys Ile Phe	Asn Ser Val Gly Asn Leu
225		230	235
Glu Arg Pro Ser	Ile Ser His	Ser Cys Gly	Gln Gly Leu Asp Glu Ala
	245	250	255
Ala Ala Tyr Ile	Lys Gly Arg	Leu Ser Pro	Ile Val Lys Ala Glu Arg
260		265	270
Ile Lys Val Leu	Val Lys Asp	Glu His Glu	Glu Val Lys Glu Leu Leu
275		280	285
Gln Glu Gly Tyr	Glu Glu Ile	Val Gly Glu	Ser Pro Ser Phe Asn Leu
290		295	300
Ala Gln Glu Ala	Trp Glu Lys	Ala Glu Arg	Arg Ala Lys Gly Gln Ser

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305              310              315              320
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
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Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
              340              345              350
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
              355              360              365
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
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Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
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<220>
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<222> (5)..(601)

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<400> 49

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gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
              20              25              30

cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
              35              40              45

agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
              50              55              60

act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
        65              70              75

ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
        80              85              90              95

tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
              100              105              110

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gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385  
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile  
                   115                                  120                                  125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433  
 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val  
                   130                                  135                                  140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481  
 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg  
                   145                                  150                                  155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529  
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr  
 160                                  165                                  170                                  175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577  
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln  
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gaa tca caa aaa gac gag ctt taa agcaaagtcc 611  
 Glu Ser Gln Lys Asp Glu Leu  
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Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu  
                   20                                  25                                  30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser  
                   35                                  40                                  45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr  
                   50                                  55                                  60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu  
                   65                                  70                                  75                                  80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys  
                                   85                                  90                                  95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala  
                   100                                  105                                  110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe  
                   115                                  120                                  125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys  
                   130                                  135                                  140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro  
145 150 155 160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala  
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Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu  
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cca tgt aga ggc ggc tca atc act gga tct cta cgt gac cgt cga ccg 96  
Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro  
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acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144  
Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg  
35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192  
Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240  
Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
65 70 75 80

caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288  
Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
85 90 95

ggg gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336  
Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu  
100 105 110

att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384  
Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys  
115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
130 135 140	
att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga	912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa	960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104

Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr  
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 gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152  
 Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser  
 370 375 380  
 tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag 1200  
 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys  
 385 390 395 400  
 aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248  
 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu  
 405 410 415  
 cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296  
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr  
 420 425 430  
 ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344  
 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His  
 435 440 445  
 cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392  
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 35 40 45  
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60  
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80  
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95  
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

[illegible]



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His Leu Val	Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr				
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Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His					
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Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg					
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&lt;211&gt; 771

&lt;212&gt; DNA

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(537)

&lt;400&gt; 53

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Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp	
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aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct	144
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro	
35 40 45	
caa gtt agt tgc aac cct ctt cgg atg cgt gag atg cgt aat ttc gat	192
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp	
50 55 60	
aat gat tgc gta ggg agt gtg gat ttt atc gag ttc atc aat gga cgt	240
Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg	
65 70 75 80	
tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca	288
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala	
85 90 95	
ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag	336
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu	
100 105 110	
tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat	384
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn	
115 120 125	
cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac	432
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp	

130 135 140  
 ggg gat ggt cga ggt gcg aaa aac agc ttt gag gaa ttt tac ggt cgt 480  
 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg  
 145 150 155 160  
 ttg cca gct acc gta cgt cgg cgt ccg tac cgt acg ttg gta agc ggt 528  
 Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly  
 165 170 175  
 gat gtg taa agttcagtcg accgtgaccg tgagcctgga agcctgaacg 577  
 Asp Val  
 ctgacaagcc cttaagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637  
 ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697  
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 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp  
 50 55 60  
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg  
 65 70 75 80  
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala  
 85 90 95  
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu  
 100 105 110  
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn  
 115 120 125  
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp  
 130 135 140  
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 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val  
 15 20 25 30

ggc ttc ggc gac gca atc ttc tac gag tcg ttc gcc ggg gat ttt gat 147  
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp  
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tcg gat tcg gcc aag 195  
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys  
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243  
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg  
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291  
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp  
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339  
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp  
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387  
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp  
 115 120 125

aaa ttt gac agc tcc acc atg ttt ggt gct gct aag tat ggc gcg agg 435  
 Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg  
 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483  
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu  
 145 150 155

tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa	531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
160 165 170	
gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat	675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
210 215 220	
ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc	723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
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atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
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gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa	867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
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aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
305 310 315	
aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa	1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata gcc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	

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 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His  
 385 390 395  
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 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro  
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 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe  
 415 420 425 430  
 tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347  
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys  
 435 440 445  
 cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395  
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser  
 450 455 460  
 att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443  
 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys  
 465 470 475  
 aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491  
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu  
 480 485 490  
 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539  
 Gly Thr Gln Asp Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala  
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 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala  
 50 55 60

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro  
 65 70 75 80  
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg  
 85 90 95  
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly  
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 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe  
 115 120 125  
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr  
 130 135 140  
 Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val  
 145 150 155 160  
 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro  
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 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu  
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 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp  
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 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser  
 210 215 220  
 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser  
 225 230 235 240  
 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu  
 245 250 255  
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys  
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 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp  
 275 280 285  
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala  
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 Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr  
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 Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys  
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 Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala  
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 Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile  
 355 360 365

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr  
370 375 380

Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu  
385 390 395 400

Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr  
405 410 415

Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser  
420 425 430

Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys  
435 440 445

Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn  
450 455 460

Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln  
465 470 475 480

Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr  
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<211> 1281

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<213> Arabidopsis thaliana

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<221> CDS

<222> (13)..(1266)

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cgg gtg acc agg gac ggt tcg ggg ccc gga aaa acc ggt gtc aca cgc 99

Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg

15

20

25

ggg tcg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147

Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly

30

35

40

45

gca tcg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195

Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile

50

55

60

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Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Tyr	Ala	Val	Ser	Ala	Lys	Phe	Pro	
			65					70					75			
aga	tta	agt	aat	aag	ggc	aaa	gat	tac	atg	cgt	tgc	gtc	ctc	caa	tac	291
Arg	Leu	Ser	Asn	Lys	Gly	Lys	Asp	Tyr	Met	Arg	Cys	Val	Leu	Gln	Tyr	
			80					85				90				
acc	gtc	aaa	aat	gaa	caa	aaa	gtt	gat	tgt	ggg	ggc	tca	tat	atc	aag	339
Thr	Val	Lys	Asn	Glu	Gln	Lys	Val	Asp	Cys	Gly	Gly	Ser	Tyr	Ile	Lys	
		95					100				105					
tta	tta	cct	tcg	aaa	ttg	cgc	acg	ggg	gat	ggg	gat	ggc	gtg	tca	gaa	387
Leu	Leu	Pro	Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	
110					115					120					125	
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Tyr	Ser	Ile	Met	Phe	Gly	Pro	Asp	Ser	Thr	Gly	Ala	Ser	Arg	Thr	Val	
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Gln	Asn	Lys	Val	Glu	Thr	Asp	Gln	Leu	Thr	His	Gln	Tyr	Thr	Thr	Ser	
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Trp	Ser	Pro	Asp	Trp	Thr	Tyr	Asn	Val	Leu	Val	Asp	Asn	Lys	Glu	Ser	
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Gln	Ala	Gly	Asn	Leu	Ala	Asp	Asp	Cys	Glu	Leu	Leu	Pro	Gln	Lys	Arg	
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Ile	Phe	Arg	Pro	Ser	Cys	Arg	Lys	Gln	Ser	Lys	Pro	Val	Thr	Cys	Val	
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Asp	Val	Lys	His	His	Ala	Pro	Arg	Arg	Asn	Val	Lys	Pro	Ala	Gly	His	
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Asp	Asp	Ile	Pro	Ala	Arg	Arg	Thr	Thr	Pro	Glu	Ala	Val	Arg	Lys	Gly	
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Arg	Thr	Asn	Glu	Arg	Pro	Asp	Arg	Thr	Trp	Ala	Thr	Gly	Thr	Thr	Pro	
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Arg	Pro	Arg	Arg	Tyr	Lys	Gly	Glu	Thr	Lys	Ala	Lys	Lys	His	Pro	Arg	
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 Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala Gly Thr Arg  
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 Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly Thr Gly Ile  
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 Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu Thr Thr Val  
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Gly Phe Phe Tyr Ser Lys Lys Ser Ser Gly Ser Asn Val Arg Glu Arg
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 Asp Ile Asp Arg Lys Asn Glu  
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caa aca gct gcc att ttg aaa atg caa gga gcc caa ctt gct gag cta 4129  
 Gln Thr Ala Ala Ile Leu Lys Met Gln Gly Ala Gln Leu Ala Glu Leu  
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gaa ata ctt tat aag gaa gaa caa gtt tta agg aaa aga tac tat aat 4177  
 Glu Ile Leu Tyr Lys Glu Glu Gln Val Leu Arg Lys Arg Tyr Tyr Asn  
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att aga gtt tat tgt cga ata aga cct cta aat gaa aaa gag agt tca 4329  
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 Tyr Leu Val Gln Ser Ala Val Asp Gly  
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 Phe Ser Leu Lys  
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 1160 1165 1170 1175

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 u Tyr Ala  
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Ser Gly Thr Asp Phe Asp Ala Glu Ser Ser Ser Leu Pro Pro Leu Ser

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Ile	Pro	Leu	Ile	Asp	Arg	Phe	Gln	Val	Glu	Ala	Phe	Leu	Arg	Leu	Met
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Gln	Lys	Gln	Ile	Gln	Ser	Ala	Gly	Lys	Arg	Gly	Phe	Phe	Tyr	Ser	Lys
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Lys	Ser	Ser	Gly	Ser	Asn	Val	Arg	Glu	Arg	Phe	Thr	Phe	Glu	Asp	Met
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Leu	Cys	Phe	Gln	Lys	Asn	Met	Ser	Leu	Ser	Pro	Ser	Phe	Leu	Gln	Asp
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Pro	Ile	Pro	Thr	Ser	Leu	Leu	Lys	Ile	Asn	Ser	Asp	Leu	Val	Ser	Arg
	130					135					140				
Ala	Thr	Lys	Leu	Phe	His	Leu	Ile	Leu	Lys	Tyr	Met	Gly	Val	Asp	Ser
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Ser	Asp	Arg	Ser	Thr	Pro	Pro	Ser	Leu	Asp	Glu	Arg	Ile	Asp	Leu	Val
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Gly	Lys	Leu	Phe	Lys	Lys	Thr	Leu	Lys	Arg	Val	Glu	Leu	Arg	Asp	Glu
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Leu	Phe	Ala	Gln	Ile	Ser	Lys	Gln	Thr	Arg	His	Asn	Pro	Asp	Arg	Gln
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Pro	Pro	Ser	Lys	Asp	Ile	Gly	Gly	Tyr	Leu	Ser	Glu	Tyr	Ile	His	Asn
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Val	Ala	His	Asp	Ala	Thr	Ile	Glu	Pro	Asp	Ala	Gln	Val	Leu	Ala	Val
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Leu	Thr	Thr	Ile	Val	Phe	Phe	Leu	Asp	Glu	Thr	Phe	Glu	Glu	Ile	Ser
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Ile	Lys	Leu	Ser	Ala	Phe	Ser	Ser	Phe	Ser	Leu	Phe	Glu	Cys	Arg	Lys
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132

173



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Tyr Gly Gln Thr Gly Ser Gly Lys Thr Phe Thr Ile Tyr Gly His Glu			
	980	985	990
Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile			
	995	1000	1005
Leu Lys Arg Asp Ser Lys Arg Phe Ser Phe Ser Leu Lys Ala Tyr Met			
	1010	1015	1020
Val Glu Leu Tyr Gln Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser			
	025	1030	1035
Ala Arg Arg Leu Lys Leu Glu Ile Lys Lys Asp Ser Lys Gly Met Val			
	1045	1050	1055
Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu Glu Leu			
	1060	1065	1070
Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser Gly Thr			
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Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser Val Val			
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Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly Lys Leu			
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Ala Leu Gly Asp Val Ile Gly Ala Leu Ser Ser Gly Asn Gln His Ile			
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Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly			
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Gly Asn Ala Lys Thr Leu Met Phe Val Asn Val Ser Pro Ala Glu Ser			
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Lys	Lys	Ala	Arg	Ser	Arg	Leu	Glu	Thr	His	Pro	Arg	Asp	Asn	Glu	Asn	
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Asn	Tyr	Arg	Leu	Ala	Thr	Ser	Ala	Gly	Thr	Lys	Gly	Gly	Ala	Arg	Thr	
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Val	Asp	Val	Pro	Val	Ile	Leu	Ser	Thr	Arg	Glu	Ser	Gln	Gly	Thr	Arg	
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Ser	Val	Asn	Ala	Thr	Ser	Lys	Ile	Arg	Cys	Pro	Asp	Ser	Thr	Ala	Ile	
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tgc	gag	tgg	ttc	gcc	acg	ccc	acg	gat	cct	caa	aga	cca	gga	gtt	tat	432
Cys	Glu	Trp	Phe	Ala	Thr	Pro	Thr	Asp	Pro	Gln	Arg	Pro	Gly	Val	Tyr	
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Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser	
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Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
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Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn	
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Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala	
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Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg	
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His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu	
275 280 285	
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Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
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Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His	
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Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr	
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 35                      40                      45  
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 50                      55                      60  
 Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn  
 65                      70                      75                      80  
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 85                      90                      95  
 Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg  
 100                      105                      110  
 Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile  
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 Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr  
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 Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn  
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 Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

139

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500										505										510																																			
Glu	Lys	His	Arg	Leu	Gln	Ile	Pro	Arg	Gln	Asn	Leu	Ala	Val	Tyr	Asn				Glu	Lys	His	Arg	Leu	Gln	Ile	Pro	Arg	Gln	Asn	Leu	Ala	Val	Tyr	Asn			Glu	Lys	His	Arg	Leu	Gln	Ile	Pro	Arg	Gln	Asn	Leu	Ala	Val	Tyr	Asn			
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ccc	gcc	ctt	tca	gaa	act	ata	ctg	aaa	gag	gga	aga	aat	aac	gga	aaa	292
Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys	
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Gly	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Cys	Ala	Leu	Ser	Lys	
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Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn	
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Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
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Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
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Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
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Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
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Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
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Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

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150

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		20						25					30		
Arg	Gln	Arg	His	Lys	Met	Gly	Ala	Asp	Asp	Phe	Glu	Pro	Leu	Thr	Met
		35					40					45			
Ile	Gly	Lys	Gly	Ala	Phe	Gly	Glu	Val	Arg	Ile	Cys	Arg	Glu	Lys	Gly
	50					55					60				
Thr	Gly	Asn	Val	Tyr	Ala	Met	Lys	Lys	Leu	Lys	Lys	Ser	Glu	Met	Leu
65					70					75					80
Arg	Arg	Gly	Gln	Val	Val	Glu	His	Val	Lys	Ala	Glu	Arg	Asn	Leu	Leu
				85					90					95	
Ala	Glu	Val	Asp	Ser	Asn	Cys	Ile	Val	Lys	Leu	Tyr	Cys	Ser	Phe	Gln
			100					105					110		
Asp	Glu	Glu	Tyr	Leu	Tyr	Leu	Ile	Met	Glu	Tyr	Leu	Pro	Gly	Gly	Asp
		115					120					125			
Met	Met	Thr	Leu	Leu	Met	Arg	Lys	Asp	Thr	Leu	Thr	Glu	Asp	Glu	Ala
		130				135						140			
Arg	Phe	Tyr	Ile	Gly	Glu	Thr	Val	Leu	Ala	Ile	Glu	Ser	Ile	His	Lys
145					150					155					160
His	Asn	Tyr	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Leu	Leu	Leu	Asp
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<400> 71

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Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
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cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
30           35           40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
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agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
60           65           70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
75           80           85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
90           95           100           105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
110           115           120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
125           130           135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
140           145           150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
155           160           165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp  
 115 120 125  
 Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro  
 130 135 140  
 Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp  
 145 150 155 160  
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu  
 165 170 175  
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly  
 180 185 190  
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr  
 195 200 205  
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser  
 210 215 220  
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys  
 225 230 235 240  
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 Met Lys Arg Leu Ser  
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agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165
Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
      10                      15

ccatctttgt tctttctact ttttgctaat gtcagacaaa acccatgtga tcctttcttc 225

actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
      sp Ser Phe Gly Tyr Thr Thr Asp Glu
      20                      25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
      30                      35                      40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
      45                      50                      55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
      60                      65                      70                      75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471
Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
      80                      85                      90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
      95                      100                      105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
      110                      115                      120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
      125                      130                      135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
      140                      145                      150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgcag att agt aaa atc aaa gct aag gta 773
      Ile Ser Lys Ile Lys Ala Lys Val
      155                      160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
      165                      170                      175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
      180                      185                      190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr  
 195 200 205 210

gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct 965  
 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser  
 215 220 225

tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013  
 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser  
 230 235 240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061  
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe  
 245 250 255

tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109  
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 260 265 270

agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157  
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser  
 275 280 285 290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203  
 Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr  
 295 300

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&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 74

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 20 25 30

Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala  
 35 40 45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser  
 50 55 60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys  
 65 70 75 80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu  
 85 90 95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln  
 100 105 110



Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly  
           115                          120                          125  
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu  
           130                          135                          140  
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala  
   145                          150                          155                          160  
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu  
                           165                          170                          175  
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser  
                           180                          185                          190  
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser  
           195                          200                          205  
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala  
           210                          215                          220  
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr  
   225                          230                          235                          240  
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly  
                           245                          250                          255  
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp  
                           260                          265                          270  
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro  
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                           15                          20                          25  
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tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt	195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg	
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gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt	243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
60 65 70	
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Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc	339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat	387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
110 115 120	
tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt	435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
125 130 135	
gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct	483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
140 145 150	
gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc	531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
155 160 165 170	
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Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
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Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
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Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct	819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

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Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn			
270	275	280	
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Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly			
285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att			963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile			
300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc			1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr			
315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct			1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala			
335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac			1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr			
350	355	360	
ggg gca gcg cca tga			1122
Gly Ala Ala Pro			
365			

&lt;210&gt; 76

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

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	20							25					30		

Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala	Leu	Gln	Gln	Met	Asn	Arg
	35						40					45			

Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg	Glu	Leu	Ser	Leu	Ile	Ser
	50					55					60				

Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly	Tyr	Arg	Leu	Ala	Arg	Leu
65					70					75				80	

Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His	Arg	Asp	Gly	Gln	Pro	Glu
			85						90					95	

Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser	Tyr	Phe	Glu	Thr	Gly	Leu
			100					105						110	

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 115 120 125  
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu  
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 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val  
 145 150 155 160  
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp  
 165 170 175  
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp  
 180 185 190  
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val  
 195 200 205  
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu  
 210 215 220  
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu  
 225 230 235 240  
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg  
 245 250 255  
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser  
 260 265 270  
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro  
 275 280 285  
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg  
 290 295 300  
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro  
 305 310 315 320  
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys  
 325 330 335  
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr  
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&lt;210&gt; 77

&lt;211&gt; 1650

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

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 15 20 25

gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa 149  
 Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys  
 30 35 40

cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc 197  
 Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala  
 45 50 55

aat gcg gtaatatact tgaccctgct ttttcttttt ccttttcttt gttacaatgg 253  
 Asn Ala  
 60

gattcgaatg atgtaactgg tttctgtttg tgccgcag gat gtg gat gtt tgt aac 308  
 Asp Val Asp Val Cys Asn  
 65

ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac 356  
 Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr  
 70 75 80

cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat 404  
 Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp  
 85 90 95

gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att 452  
 Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile  
 100 105 110 115

caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct 502  
 Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly  
 120 125

tacccaaaga agcataaaag caattcacta gcctgattct tctttcttct cctcttttgt 562

actagtagca tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671  
Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe  
130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719  
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro  
140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767  
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr  
155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815  
Glu Phe Ala Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala  
175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868  
Leu Thr Ala Phe Ile Phe Gly Ar  
190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acctatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt ttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044  
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agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092  
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg  
195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140  
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr  
215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188  
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly  
230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236  
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His  
245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284  
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu  
260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332  
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly  
275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380  
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile  
295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428  
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg  
                   310                  315                  320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476  
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr  
                   325                  330                  335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524  
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile  
                   340                  345                  350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572  
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn  
                   355                  360                  365                  370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625  
 Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro  
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ctttgtgaga ctattgccaa gttag 1650

<210> 78

<211> 380

<212> PRT

<213> Arabidopsis thaliana

<400> 78

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                   20                  25                  30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu  
                   35                  40                  45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp  
                   50                  55                  60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu  
                   65                  70                  75                  80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe  
                   85                  90                  95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly  
                   100                  105                  110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp  
                   115                  120                  125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu  
                   130                  135                  140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala  
 145 150 155 160  
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser  
 165 170 175  
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe  
 180 185 190  
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu  
 195 200 205  
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn  
 210 215 220  
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr  
 225 230 235 240  
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp  
 245 250 255  
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu  
 260 265 270  
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile  
 275 280 285  
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val  
 290 295 300  
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys  
 305 310 315 320  
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn  
 325 330 335  
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile  
 340 345 350  
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<400> 79



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gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
              15              20              25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
              30              35              40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
              45              50              55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
              60              65              70              75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
              80              85              90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
              95              100              105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
              110              115              120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
              125              130              135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
              140              145              150              155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
              160              165              170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
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gaagattatc attaa      590

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<210> 80
<211> 185
<212> PRT
<213> Arabidopsis thaliana

<400> 80

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 20 25 30

Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile  
 35 40 45

Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu  
 50 55 60

Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser  
 65 70 75 80

Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys  
 85 90 95

Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu  
 100 105 110

Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly  
 115 120 125

His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val  
 130 135 140

Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile  
 145 150 155 160

Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr  
 165 170 175

Val Glu Glu Glu Lys Lys Asp Lys Glu  
 180 185

<210> 81  
 <211> 1376  
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 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys  
 15 20 25

tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
	30						35					40					
gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggg	gtg	ata	ggg	tca	gtg	ttc	196	
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50				55							
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244	
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
	60				65				70					75			
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292	
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
			80						85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340	
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys		
			95					100					105				
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggg	gag	tat	aaa	gac	tat	388	
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr		
	110					115						120					
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436	
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala		
	125					130						135					
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484	
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
	140				145					150					155		
aag	acg	gcg	gag	aag	att	ggg	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532	
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys		
			160						165					170			
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580	
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser		
			175					180						185			
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628	
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
		190					195						200				
aag	gtt	ggg	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676	
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
	205					210					215						
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724	
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
	220				225					230					235		
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772	
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
			240						245					250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820	
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala		

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu 270 275 280			868
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn 285 290 295			916
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg 300 305 310 315			964
ttg gaa ggt aaa gag ctg aaa gaa gaa gct gga gca aaa gcc caa gag Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu 320 325 330			1012
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala 335 340 345			1060
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly 350 355 360			1108
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys 365 370 375			1156
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu 380 385 390 395			1204
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser 400 405 410			1252
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr 415 420 425			1300
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys 430 435 440			1348
gat aag gga aag ctg tga gaataactaga Asp Lys Gly Lys Leu 445			1376

&lt;210&gt; 82

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 82

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 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu  
 35 40 45  
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly  
 50 55 60  
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala  
 65 70 75 80  
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val  
 85 90 95  
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr  
 100 105 110  
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala  
 115 120 125  
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn  
 130 135 140  
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys  
 145 150 155 160  
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys  
 165 170 175  
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp  
 180 185 190  
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr  
 195 200 205  
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala  
 210 215 220  
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu  
 225 230 235 240  
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr  
 245 250 255  
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys  
 260 265 270  
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys  
 275 280 285  
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly  
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu  
 305 310 315 320  
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr  
 325 330 335  
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp  
 340 345 350  
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala  
 355 360 365  
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser  
 370 375 380  
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly  
 385 390 395 400  
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val  
 405 410 415  
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn  
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 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu  
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<210> 83  
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 <212> DNA  
 <213> Arabidopsis thaliana

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 <222> (18)..(548)

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 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr  
 15 20 25  
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146  
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln  
 30 35 40  
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194  
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly  
 45 50 55  
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242  
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

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cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggg caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

&lt;210&gt; 84

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 84

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Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp  
115 120 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg  
130 135 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val  
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Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr  
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<210> 85

<211> 988

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (12) .. (977)

<400> 85

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Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly  
15 20 25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146  
Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val  
30 35 40 45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194  
Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu  
50 55 60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242  
Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val  
65 70 75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290  
Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn  
80 85 90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338  
Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu  
95 100 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386  
Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu  
110 115 120 125



gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt	434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val	
130 135 140	
gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac	482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn	
145 150 155	
ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc	530
Leu Pro Phe Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg	
160 165 170	
tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac	578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His	
175 180 185	
aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac	626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn	
190 195 200 205	
ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc	674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala	
210 215 220	
gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta	722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu	
225 230 235	
gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg	770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr	
240 245 250	
cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc	818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu	
255 260 265	
gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat	866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His	
270 275 280 285	
ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt	914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly	
290 295 300	
cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt	962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys	
305 310 315	
cgg tct gct aat taa gagatataga aa	989
Arg Ser Ala Asn	
320	

&lt;210&gt; 86

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 86

Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu  
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 20 25 30  
 Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp  
 35 40 45  
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe  
 50 55 60  
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp  
 65 70 75 80  
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu  
 85 90 95  
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val  
 100 105 110  
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg  
 115 120 125  
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly  
 130 135 140  
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser  
 145 150 155 160  
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly  
 165 170 175  
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly  
 180 185 190  
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly  
 195 200 205  
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu  
 210 215 220  
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp  
 225 230 235 240  
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala  
 245 250 255  
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser  
 260 265 270  
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met  
 275 280 285  
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

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tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc 97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro
  15                20                25                30

cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct 145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala
      35                40                45

tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag 193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu
      50                55                60

ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt 241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe
      65                70                75

gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct 289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala
      80                85                90

aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt 337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg
      95                100                105                110

gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt 385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val
      115                120                125

aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt 433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe
      130                135                140

gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc 481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr

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145                      150                      155  
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 Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser  
 160                      165                      170  
 cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa 577  
 Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu  
 175                      180                      185                      190  
 aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc 625  
 Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser  
 195                      200                      205  
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 <212> PRT  
 <213> Arabidopsis thaliana  
  
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 20                      25                      30  
 Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu  
 35                      40                      45  
 Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val  
 50                      55                      60  
 Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala  
 65                      70                      75                      80  
 Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val  
 85                      90                      95  
 Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala  
 100                      105                      110  
 Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val  
 115                      120                      125  
 Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys  
 130                      135                      140  
 Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly  
 145                      150                      155                      160  
 Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu  
 165                      170                      175

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys  
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Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg  
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<211> 1223

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<221> CDS

<222> (16)..(1215)

<400> 89

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gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99  
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly  
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147  
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro  
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195  
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr  
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243  
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser  
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291  
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr  
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339  
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp  
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387  
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser  
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435  
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser  
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483  
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg  
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

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 385 390 395

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Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala  
 35 40 45

Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg  
 50 55 60

Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr  
 65 70 75 80

Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr  
 85 90 95

Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln  
 100 105 110

Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly  
 115 120 125

Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu  
 130 135 140

Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr  
 145 150 155 160

Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln  
 165 170 175

Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr  
 180 185 190

Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His  
 195 200 205

Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr  
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys  
 225 230 235 240  
 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val  
 245 250 255  
 Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu  
 260 265 270  
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly  
 275 280 285  
 Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp  
 290 295 300  
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp  
 305 310 315 320  
 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala  
 325 330 335  
 Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu  
 340 345 350  
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys  
 355 360 365  
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 370 375 380  
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 <211> 536  
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 <222> (12)..(524)

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 gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98  
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu  
 15 20 25  
 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146  
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr  
 30 35 40 45



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aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
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tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
      65                      70                      75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
      80                      85                      90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
      95                      100                     105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
     110                      115                      120                     125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
      130                      135                      140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
      145                      150                      155

gag aag ttt gta caa gat gat tct tct ccg gct tgg gct tga 524
Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
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agaagttggt ta 536

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<210> 92  
 <211> 170  
 <212> PRT  
 <213> Arabidopsis thaliana

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<400> 92
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Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
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Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
      35                      40                      45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
      50                      55                      60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
      65                      70                      75                      80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

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	85		90		95
Thr Asp Thr	Leu Glu Lys Lys Gln Val Glu Thr Ile Val Trp Ala Asn				
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Lys Asp Asp	Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp Lys				
	115		120		125
Arg Leu His	Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu				
	130		135		140
Trp Lys Lys	Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe				
	145		150		155
Val Gln Asp	Asp Ser Ser Pro Ala Ser Ala				
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 <211> 293  
 <212> DNA  
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 <222> (197)..(278)

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 aaa tgt ggt gat tcg tgc ag gtaaacccta gattctctct tcattaactt 101  
 Lys Cys Gly Asp Ser Cys Se  
                   15  
 atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161  
 tcttataactt ctgttggtttt ttggtatga caaag t tgc gag aag aac tac aac 215  
                                   r Cys Glu Lys Asn Tyr Asn  
                                   20                  25  
 aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263  
 Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser  
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 agc tgt aac tgt tga agaaattatc agcat 293  
 Ser Cys Asn Cys  
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<210> 94

<211> 45  
 <212> PRT  
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<210> 95  
 <211> 880  
 <212> DNA  
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<220>  
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 <222> (14)..(868)

<400> 95  
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 Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile  
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 cgc ctc aga tct ctc gct ctt tgc tct tct ttt tct tct ttc cga ttt 97  
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe  
 15 20 25  
 gcc cat cgt cct ctg tca tgc att tca ccg aga aag tta ccg aat ttt 145  
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe  
 30 35 40  
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193  
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met  
 45 50 55 60  
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241  
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val  
 65 70 75  
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289  
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His  
 80 85 90  
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337  
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser  
 95 100 105  
 gta ttt tta ttc aac tgc aag tat gag ttg ctt ctc cag caa agg tca 385  
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser  
 110 115 120

aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433  
 Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser  
 125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481  
 His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly  
 145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529  
 Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val  
 160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577  
 Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu  
 175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625  
 Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr  
 190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673  
 Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu  
 205 210 215 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721  
 Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val  
 225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769  
 Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe  
 240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817  
 Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu  
 255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865  
 Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu  
 270 275 280

tga acatcttttt tt 880  
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&lt;210&gt; 96

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 96

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Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro  
 20 25 30

Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser  
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           50                          55                          60  
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp  
   65                          70                          75                          80  
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn  
                           85                          90                          95  
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe  
                          100                         105                         110  
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val  
                          115                         120                         125  
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr  
   130                         135                         140  
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala  
 145                         150                         155                         160  
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val  
                          165                         170                         175  
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro  
                          180                         185                         190  
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile  
                          195                         200                         205  
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile  
   210                         215                         220  
 Lys Tyr Val Ser Arg Glu Leu Lys Glu Leu Val Lys Lys Ala Asp  
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 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val  
                          245                         250                         255  
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu  
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<210> 97  
 <211> 831  
 <212> DNA  
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<220>

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&lt;222&gt; (18)..(821)

&lt;400&gt; 97

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gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc	98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val	
15 20 25	
ctt gga agc gcc cgt gtg aca atg agg aag act gtt gcc aag cca aag	146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys	
30 35 40	
ggc cca tca gcc agc cca tgg tac gga tct gac cgt gtc aag tac ttg	194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu	
45 50 55	
ggt cca ttc tct gcc gaa tca ccg agc tac ctt acc gga gag ttc ccc	242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro	
60 65 70 75	
gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca	290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr	
80 85 90	
ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg	338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met	
95 100 105	
ctc gga gcc cta gcc tgc gtc ttc cct gag ctt ttg gct aga aac gga	386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly	
110 115 120	
gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc	434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe	
125 130 135	
agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct	482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala	
140 145 150 155	
cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc	530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala	
160 165 170	
gtt gaa gcc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag	578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu	
175 180 185	
gac ttg ctt tac ccc ggt gcc agc ttc gac cca ttg ggt ttg gct acc	626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr	
190 195 200	
gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga	674

Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly  
 205 210 215  
 aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722  
 Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val  
 220 225 230 235  
 act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770  
 Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro  
 240 245 250  
 gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818  
 Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys  
 255 260 265  
 tga gccaaagtttt 831

<210> 98  
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 <213> Arabidopsis thaliana

<400> 98

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 35 40 45  
 Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly  
 50 55 60  
 Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp  
 65 70 75 80  
 Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg  
 85 90 95  
 Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
 100 105 110  
 Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu  
 115 120 125  
 Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu  
 130 135 140  
 Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala  
 145 150 155 160  
 Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg  
 165 170 175

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro  
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe  
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe  
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro  
 225 230 235 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala  
 245 250 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys  
 260 265

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 <222> (257)..(305)

<220>  
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 <222> (416)..(843)

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 1 5 10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98  
 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp  
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146  
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu  
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194  
 Pro Phe Ile Leu Arg Asn  
 45 50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254



ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301  
 Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile  
 55 60 65  
 ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt 355  
 Phe G  
 atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415  
 aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462  
 lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys  
 70 75 80  
 gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510  
 Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met  
 85 90 95  
 ggc att gaa att gag tgc cat gag ttt gac cca gtt ggt tca aag ctt 558  
 Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu  
 100 105 110  
 gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606  
 Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys  
 115 120 125  
 act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654  
 Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val  
 130 135 140 145  
 tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702  
 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe  
 150 155 160  
 act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750  
 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Gly  
 165 170 175  
 act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798  
 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp  
 180 185 190  
 gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843  
 Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu  
 195 200 205  
 gtgaatctca aa 855

&lt;210&gt; 100

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 100

Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser Thr Ala Thr Arg  
 1 5 10 15

Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp Phe Glu Phe Val  
 20 25 30  
 His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu  
 35 40 45  
 Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys  
 50 55 60  
 Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser  
 65 70 75 80  
 Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile  
 85 90 95  
 Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser  
 100 105 110  
 Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr  
 115 120 125  
 Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu  
 130 135 140  
 Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp  
 145 150 155 160  
 His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu  
 165 170 175  
 Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser  
 180 185 190  
 Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu  
 195 200 205

<210> 101  
 <211> 512  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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<220>  
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 <222> (241)..(309)

<220>  
 <221> CDS  
 <222> (417)..(492)

<400> 101  
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Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln  
 1 5 10

acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact 97  
 Thr Ala Gly Lys Ala Gl  
 15

cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157

actagaaatt tcagttactt gtttaattta gttgtcgtta attatgtaatt tgatgatttt 217

atgggtacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268  
 u Glu Lys Ser Asn Val Leu Leu Asp Lys  
 20 25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319  
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl  
 30 35 40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379

gtacgcagat ttctgatatg gttatgtata tgttata g gcg gga aag agt gta 432  
 n Ala Gly Lys Ser Val  
 45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480  
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly  
 50 55 60

ctg aac aag tag agattcgggt caaatttggg 512  
 Leu Asn Lys  
 65

<210> 102

<211> 66

<212> PRT

<213> Arabidopsis thaliana

<400> 102

Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly  
 1 5 10 15

Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala  
 20 25 30

Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser  
 35 40 45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu  
 50 55 60

Asn Lys  
 65

<210> 103  
 <211> 1138  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (11)..(1123)

<400> 103  
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                   Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn  
                   1                  5                  10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97  
 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp  
           15                  20                  25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145  
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val  
           30                  35                  40                  45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193  
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys  
                   50                  55                  60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241  
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu  
                   65                  70                  75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289  
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala  
           80                  85                  90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337  
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val  
           95                  100                  105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385  
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys  
           110                  115                  120                  125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433  
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln  
                   130                  135                  140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481  
 Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg  
           145                  150                  155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529  
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys  
           160                  165                  170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577  
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe  
           175                  180                  185

atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625  
 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu  
 190 195 200 205  
 ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673  
 Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly  
 210 215 220  
 tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721  
 Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr  
 225 230 235  
 gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769  
 Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln  
 240 245 250  
 aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817  
 Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr  
 255 260 265  
 att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865  
 Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr  
 270 275 280 285  
 ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913  
 Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val  
 290 295 300  
 ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961  
 Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro  
 305 310 315  
 tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009  
 Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val  
 320 325 330  
 cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057  
 Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg  
 335 340 345  
 gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105  
 Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr  
 350 355 360 365  
 tta aac act gag ctc tga gctcaagtct tgttt 1138  
 Leu Asn Thr Glu Leu  
 370

&lt;210&gt; 104

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 104

Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn Glu Gly Lys

1	5	10	15
His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp Thr Lys Tyr	20	25	30
Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro	290	295	300
Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro Tyr Met Ala			

305                      310                      315                      320  
 Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val Pro Ile Asp  
                                  325                                   330                                   335  
 Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg Glu Met Ile  
                                  340                                   345                                   350  
 Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr Leu Asn Thr  
                                  355                                   360                                   365  
 Glu Leu  
                  370

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 <211> 445  
 <212> DNA  
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<220>  
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 <222> (20)..(430)

<400> 105  
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 gcg aag acg atg gct gct aac aag gac aaa gac aag gac aag aag aaa 100  
 Ala Lys Thr Met Ala Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys  
                                  15                                   20                                   25  
 ccc atc tct cgc tct gct cgt gct ggt att cag ttt cca gtt gga cga 148  
 Pro Ile Ser Arg Ser Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg  
                                  30                                   35                                   40  
 att cac agg caa ctg aag acc cga gtc tcg gca cat ggc aga gtt ggt 196  
 Ile His Arg Gln Leu Lys Thr Arg Val Ser Ala His Gly Arg Val Gly  
                                  45                                   50                                   55  
 gcc act gca gcc gtc tac aca gct tca atc ctg gag tat ctg aca gca 244  
 Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala  
                                  60                                   65                                   70                                   75  
 gag gtt ctt gag ttg gct ggg aat gcg agc aag gat ctc aaa gtg aag 292  
 Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys  
                                  80                                   85                                   90  
 agg ata acg cca agg cat ctg cag ttg gcg att aga gga gat gag gag 340  
 Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu  
                                  95                                   100                                   105  
 ctg gac aca ctc atc aag gga acg att gct gga ggt ggt gtg atc cct 388  
 Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro  
                                  110                                   115                                   120

cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430  
 His Ile His Lys Ser Leu Ile Asn Lys Thr Thr Lys Glu  
 125 130 135

tgtgtagctt tttat 445

<210> 106  
 <211> 136  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 106  
 Met Ala Gly Lys Gly Lys Gly Leu Val Ala Ala Lys Thr Met Ala  
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 Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys Pro Ile Ser Arg Ser  
 20 25 30  
 Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu  
 35 40 45  
 Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val  
 50 55 60  
 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu  
 65 70 75 80  
 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg  
 85 90 95  
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile  
 100 105 110  
 Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser  
 115 120 125  
 Leu Ile Asn Lys Thr Thr Lys Glu  
 130 135

<210> 107  
 <211> 930  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (14)..(916)

<400> 107  
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 Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu  
 1 5 10



tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
tgg gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat	529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg  
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 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu  
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 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro  
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Thr	Glu	Ala	Ile	Asn	Leu	Ser	Pro	Thr	Asn	His	Ile	Leu	Tyr	Ser	Asn	
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Arg	Ser	Ala	Ser	Tyr	Ala	Ser	Leu	His	Arg	Tyr	Glu	Glu	Ala	Leu	Ser	
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Asp	Ala	Lys	Lys	Thr	Ile	Glu	Leu	Lys	Pro	Asp	Trp	Ser	Lys	Gly	Tyr	
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Ser	Arg	Leu	Gly	Ala	Ala	Phe	Ile	Gly	Leu	Ser	Lys	Phe	Asp	Glu	Ala	
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Val	Asp	Ser	Tyr	Lys	Lys	Gly	Leu	Glu	Ile	Asp	Pro	Ser	Asn	Glu	Met	
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Tyr	Met	Lys	Asp	Lys	Arg	Val	Met	Lys	Ala	Leu	Gly	Val	Leu	Leu	Asn	
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Asp	Glu	Arg	Lys	Glu	Pro	Glu	Pro	Glu	Met	Glu	Pro	Met	Glu	Leu	Thr	
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 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser  
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Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly  
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Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp  
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Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala  
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Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr  
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Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile  
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Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val  
165 170 175

Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser  
180 185 190

Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu  
195 200 205

Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys  
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Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

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 ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr  
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 Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn  
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Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn Met  
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Lys	Glu	Met	Phe	Asp	Arg	Ser	Ala	Asp	Leu	Gly	Val	Glu	Asn	Ile	Val	
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Ile	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Gly	Asn	Val	Val	
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Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
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Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
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Tyr

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Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
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190                               195                               200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att 675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
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Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile	
220 225 230	
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Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
270 275 280	
ggg cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att	915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
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gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat	963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
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gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
315 320 325	
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Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
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Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser	
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Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys	
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Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val	
380 385 390	
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt	1251
Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe	
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Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln	
410 415 420 425	
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Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu	
430 435 440	
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cca

1399

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&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

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Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro  
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Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu  
 65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu  
 85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala  
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Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn  
 115 120 125

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Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg  
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His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr  
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Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val  
 195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro  
 210 215 220

Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val  
 225 230 235 240

Lys	Lys	Trp	Asn	Val	Ala	Leu	Met	Ser	Met	Ser	Ala	His	Lys	Ile	Tyr	245	250	255
Gly	Pro	Lys	Gly	Val	Gly	Ala	Leu	Tyr	Val	Arg	Arg	Arg	Pro	Arg	Ile	260	265	270
Arg	Leu	Glu	Pro	Leu	Met	Asn	Gly	Gly	Gly	Gln	Glu	Arg	Gly	Leu	Arg	275	280	285
Ser	Gly	Thr	Gly	Ala	Thr	Gln	Gln	Ile	Val	Gly	Phe	Gly	Ala	Ala	Cys	290	295	300
Glu	Leu	Ala	Met	Lys	Glu	Met	Glu	Tyr	Asp	Glu	Lys	Trp	Ile	Lys	Gly	305	310	315
Leu	Gln	Glu	Arg	Leu	Leu	Asn	Gly	Val	Arg	Glu	Lys	Leu	Asp	Gly	Val	320	325	330
Val	Val	Asn	Gly	Ser	Met	Asp	Ser	Arg	Tyr	Val	Gly	Asn	Leu	Asn	Leu	335	340	345
Ser	Phe	Ala	Tyr	Val	Glu	Gly	Glu	Ser	Leu	Leu	Met	Gly	Leu	Lys	Glu	350	355	360
Val	Ala	Val	Ser	Ser	Gly	Ser	Ala	Cys	Thr	Ser	Ala	Ser	Leu	Glu	Pro	365	370	375
Ser	Tyr	Val	Leu	Arg	Ala	Leu	Gly	Val	Asp	Glu	Asp	Met	Ala	His	Thr	380	385	390
Ser	Ile	Arg	Phe	Gly	Ile	Gly	Arg	Phe	Thr	Thr	Lys	Glu	Glu	Ile	Asp	395	400	405
Lys	Ala	Val	Glu	Leu	Thr	Val	Lys	Gln	Val	Glu	Lys	Leu	Arg	Glu	Met	410	415	420
Ser	Pro	Leu	Tyr	Glu	Met	Val	Lys	Glu	Gly	Ile	Asp	Ile	Lys	Asn	Ile	425	430	435
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ctt ctt tct tgt ttt ctc caa gtt tct tcc aat gga gac gct gag ata	97
Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile	
15 20 25 30	
ttg agt aga gtt aaa aag acc cga ctt ttc gac ccc gat gga aat tta	145
Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu	
35 40 45	
caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg	193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr	
50 55 60	
gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc	241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr	
65 70 75	
att gat ctc tcc ggc tat aat atc tcc ggt ggc ttt ccc tac gga ttc	289
Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe	
80 85 90	
tgt cgt atc cgt aca ctc atc aac atc act ctt tct caa aac aat ctc	337
Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu	
95 100 105 110	
aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag	385
Asn Gly Thr Ile Asn Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln	
115 120 125	
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Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe	
130 135 140	
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Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln	
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Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe	
175 180 185 190	
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195 200 205	

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act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp 225 230 235	721
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn 240 245 250	769
agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val 255 260 265 270	817
tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu 275 280 285	865
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aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile 305 310 315	961
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gaa ttc gat gtc tcg acg aac aga ttc tcc ggt gaa ttg ccg ccg tat Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr 370 375 380	1153
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cag ctt gaa atc tcc gct aac aac ttc tcc ggt gtg att ccc gtc aaa	1441
Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
465 470 475	
ctt tgt gat ctc cgt gat ctc aga gtc atc gat ctt agc cgc aac agt	1489
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Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu	
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Tyr G ly	
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Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
625 630 635 640	
tta ttc aag aga aaa ccg aaa ccg acc aac aaa ata acc atc ttc cag	2026
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 Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp  
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 Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly  
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 820 825 830

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 835 840 845

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 Ala Pro G  
 850

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 855



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                     355                    360                    365  
 Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr Leu Cys  
                     370                    375                    380

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 Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn Tyr Ile  
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 Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val  
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 Ala Pro Glu Tyr Gly Tyr Thr Ser Lys Val Asn Glu Lys Ser Asp Val  
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 Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Lys Arg Pro  
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 Glu Ala Ala Leu Cys Tyr Pro Ser Pro Ser Ala Glu Asp Gly Ala Met  
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